Claims

1. Genetically modified bacteria **characterized** by the fact that it can have flocculation genes regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

2. Genetically modified fungus **characterized** by the fact that it can have flocculation genes regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

3. Genetically modified archae **characterized** by the fact that it can have flocculation genes regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

4. Genetically modified yeast **characterized** by the fact that it can have one or more of the flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

5. Genetically modified yeast **characterized** by the fact that it can have the flocculation gene FLO10 regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

6. Genetically modified yeast, preferrably *Pichia pastoris*, *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

7. Genetically modified yeast, preferrably *Pichia pastoris*, *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have the flocculation gene, FLO10, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

8. Genetically modified yeast *Saccharomyces cerevisiae* from one of the lines below:

956. X2180-1A, ATCC 26786 a SUC2 mal gal2 CUP1 R. K. Mortimer

957. X2180-1B, ATCC 26787 alpha SUC2 mal gal2 CUP1 R. K. Mortimer

857. 158 a *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart

858. 159 alpha *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart

713. KIL-k2 From draught beer) Antonie van Leeuwenhoek, 1978, 44, 59 M. Richards

738. KIL-k2 (brewery contaminant) Antonie van Leeuwenhoek, 1978, 44, 59 A. P. Maule

761. KIL-k3 From palm wine), CBS 7903 *J. Ferm. Technol.*, 1985, 63, 421-429 N. Okafor

1001. KIL-k2 (brewing yeast) Antonie van Leeuwenhoek, 1978, 44, 59

1561. A8209B his4-864 KIL-k1 G. Fink via T. Young

958. X2928-3D-1A a ade1 gal1 leu1 his2 ura3 trp1 met14 R. K. Mortimer

959. X2928-3D-1C alpha ade1 gal1 leu1 his2 ura3 trp1 met14 R. K. Mortimer

1786. STX 147-4C alpha ade1 his7 tyr1 gal1 cly8 ade5 aro2 met13 lys5 trp5 cyh2 arg4 lys1 ura4 gal2 ade2 rad56 L. Johnston

1620. STX77-6C alpha gal1 his4 trp1 hom3 ura3 CUP1 ilv3 ade3 rad52 rna1 L. Johnston

1618. X4119-19C a his7 tyr1 cdc9 trp4 aro1B hom2 rad2 thr1 lys11 gal2 ade2 L. Johnston

1661. X4120-19D alpha lys2 leu2 pet14 rad(?) rna3 ade8 aro1D met10 ade5 leu1 CUP1 L. Johnston

1619. STX66-4A a rad18 lys4 trp1 prt3 CUP1 gal2 ade2 met2 pha2 L. Johnston

1617. K396-22B alpha spo11 ura3 ade1 his1 leu2 lys7 met3 trp5 L. Johnston

1614. K381-9D alpha spo11 ura3 ade6 arg4 aro7 asp5 met14 lys2 pet17 trp1 L. Johnston

1613. K398-4D a spo11 ura3 ade6 arg4 aro7 asp5 met14 lys2 pet17 trp1 L. Johnston

1611. K382-23A a spo11 ura3 can1 cyh2 ade2 his7 hom3 L. Johnston

1612. K382-19D alpha spo11 ura3 can1 cyh2 ade2 his7 hom3 tyr1 L. Johnston

1616. K393-35C alpha spo11 ura3 his2 leu1 lys1 met4 pet8 L. Johnston

1615. K399-7D a spo11 ura3 his2 leu1 lys1 met4 pet8 L. Johnston

1383. DBY 747, ATCC 44774 a leu2-3 leu2-112 his3-DELTA1 trp4-289 ura3-52 *Gene*, 1979, 8, 17-24. J. F. Makins

1392. MC16 alpha leu2-3 his4-712FS) SUF2 ade2-1 lys2-1 *Nature*, 1981, 275, 104. J. F. Makins

1445. LL20 alpha his3-11 his3-15 leu2-3 leu2-112 *J. Bacteriol.*, 1979, 140, 73-82 A. Coddington

1527. MD40/4C alpha leu2-3 leu2-112 his3-11 his3-15 ura2 trp1 CAN s B. Bowen

1528. AH22 a leu2-3 leu2-112 his4 canR B. Bowen

1627. D13-1A (YNN6) a trp1 his3-532 gal2 L. Johnston

1771. cdc9-1 (L89-6C) a cdc9-1 leu2 ade1 ade2 ura1 lys2 L. Johnston

804. D160 a ura3 his1 arg6 trp2 ade1 J. F. T. Spencer

805. A364A a ade1 ade2 ura1 his7 lys2 tyr1 gal1 *J. Mol. Biol.*, 1976, 105, 427-443 J. F. T. Spencer

806. x112 alpha ade8-2 trp5-2 lys2-1 ura1-1 J. F. T. Spencer

808. GRH1 a trp1 ade1 his7 ura1 gal1 G. Stewart

1395. S1896D a met7 trp1 leu1 ade1 gal1 gal2 pet R. K. Mortimer

1396. F33 alpha met7 gal2 pet R. K. Mortimer

1623. X2181-1B a gal1 his2 trp1 ade1
1626. CG379 ade+ alpha his7-2 leu2-3 leu2-112 trp1-289 ura3-52 (ade5 rev)
1631. g440-7C alpha ade4 trp1 L. Johnston
1632. D273-11A alpha ade1 his1 trp2 L. Johnston
1662. alpha arg met L. Johnston
1663. a arg met L. Johnston
1664. alpha/alpha arg 2μ + L. Johnston
1719. A364A rho- a ade1 ade2 ura1 his7 lys2 tyr1 gal1 rho- L. Johnston
1720. B635 a cyc1-115 his1-1 lys2-1 trp2 L. Johnston
1772. L126-R9 a leu2 hom3-10 his1 L. Johnston
1790. a/a arg his 2μ + L. Johnston
1812. L126-2B a leu2 hom3-10 his1 L. Johnston
1821. S13 a his4 ura1 trp5 gal2 L. Johnston
1822. S49 a his4 ura1 trp5 gal2 ade6 L. Johnston
1961. GRF18 alpha leu2-3 leu2-212 his3-11 his3-15 canR G. Fink via D. MacKenzie
1356. A 137 alpha pho80-2 *J. Bacteriol.*, 1973, 113, 727-738 A. Coddington
1357. A 138 a pho80-2 *J. Bacteriol.*, 1973, 113, 727-738 A. Coddington
828. a ade1 J. F. T. Spencer
829. alpha ade1 J. F. T. Spencer
1577. a ade1 leu1 B. Pearson
1652. a ade1 leu2 B. Pearson
830. a ade2 J. F. T. Spencer
802. alpha ade2 (lys) J. F. T. Spencer
832. a ade3 J. F. T. Spencer
833. alpha ade3 (ura) J. F. T. Spencer
834. a ade4 J. F. T. Spencer
835. alpha ade4 (ura) J. F. T. Spencer
836. a ade5 J. F. T. Spencer
837. alpha ade5 (ura) J. F. T. Spencer
838. a ade6 J. F. T. Spencer
839. alpha ade6 (trp) J. F. T. Spencer
840. a ade7 J. F. T. Spencer
841. alpha ade7 J. F. T. Spencer
842. a ade8 J. F. T. Spencer
843. alpha ade8 (lys trp) J. F. T. Spencer
1654. cdc3-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc3-1 L. Johnston
1642. cdc4-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc4-1 L. Johnston
1643. cdc5-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc5-1 L. Johnston

1723. cdc6-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc6-1 L. Johnston
1729. cdc7-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc7-1 L. Johnston
1730. cdc8-141 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc8-141 L. Johnston
1667. cdc8-198 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc8-198 L. Johnston
1771. cdc9-1 (L89-6C) a cdc9-1 leu2 ade1 ade2 ura1 lys2 L. Johnston
1788. cdc9-1 rev1 cdc9-1 rev1 L. Johnston
1672. cdc9-12 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-12 L. Johnston
1673. cdc9-13 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-13 L. Johnston
1791. cdc9-3 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-3 2μ+ L. Johnston
1731. cdc9-4 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-4 L. Johnston
1732. cdc9-6 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-6 L. Johnston
1807. cdc9-7 (L82-2B) a cdc9-7 trp1 lys2 his7 L. Johnston
1808. cdc9-7 (L94-4D) a cdc9-7 trp1 ura3 L. Johnston
1670. cdc9-7 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-7 L. Johnston
1633. cdc9-7 rho- cdc9-7 rho- L. Johnston
1671. cdc9-8 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-8 L. Johnston
1674. cdc10-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc10-1 L. Johnston
1655. cdc11-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc11-1 L. Johnston
1733. cdc12-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc12-1 L. Johnston
1734. cdc13-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc13-1 L. Johnston
1735. cdc14-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc14-1 L. Johnston
1736. cdc18-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc18-1 L. Johnston
1737. cdc19-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc19-1 L. Johnston
1738. cdc26-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc26-1 L. Johnston
1665. cdc28-4 L31-7a a cdc28-4 tyr1 L. Johnston
1675. cdc30-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc30-1 L. Johnston
1676. cdc31-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc31-1 L. Johnston
1722. cdc36-16 SR661-2 a cdc36-16 trp1-1 ura1 L. Johnston
1666. cdc37-1 SR672-1 a cdc37-1 ura1 cyh2 L. Johnston
1641. cdc39-1 SR665-1 alpha cdc39-1 met2 tyr1 cyh2 L. Johnston
1677. cdc41 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc41 L. Johnston
1753. cdc6 (MH18) cdc6/cdc6 gal1/gal1 ade1/ade1 +/ade2 his1/his7 trp2/+ +/ura1 +/lys2 +/tyr1 2μ+ L. Johnston
1754. cdc13 (MH20) cdc13/cdc13 gal1/gal1 ade1/ade1 +/ade2 his1/his7 trp2/+ +/ura1 +/lys2 +/tyr1 2μ+ L. Johnston
1752. cdc15-1 (MH15) cdc15-1/cdc15-1 gal1/gal1 ade1/ade1 +/ade2 his1/his7 trp2/+ +/ura1 +/lys2 +/tyr1 2μ+ L. Johnston
1755. cdc17 (MH21) cdc17/cdc17 gal1/gal1 ade1/ade1 +/ade2 his1/his7 trp2/+ +/ura1

+/lys2 +/tyr1 2μ+ L. Johnston

1756. cdc21 (MH21) cdc21/cdc21 gal1/gal1 ade1/ade1 +/ade2 his1/his7 trp2/+ +/ura1 +/lys2 +/tyr1 2μ+ L. Johnston

1718. JC2 (L31-9a [a]/L31-2c [alpha]) cdc9/cdc9 cdc28/cdc28 ade/+ tyr1/tyr/1 canR/+ +/his1 L. Johnston

1797. cdc36(MH30) alpha/a gal1/gal1 ade1/+ his1/+ trp2/+ +/trp1 +/ura1

961. 2C-4 alpha arg4-2/+ arg4-17/+ CUP1/+ thr1/+; rec5 leu1 trp5 trp1 his5 ade2 *Radiation Res.*, 1972, 49, 133 & 148 R. K. Mortimer

960. 2C-8 alpha arg4-2/+ arg4-17/+ CUP1/+ thr1/+; rec4 leu1 trp5 trp1 his5 ade2 *Radiation Res.*, 1972, 49, 133 & 148 R. K. Mortimer

1823. dbf1 (L123-8A) alpha trp1 ura3 dbf1 L. Johnston

1824. dbf2 (L119-7D) alpha trp? ura3 ade1 dbf2 L. Johnston

1750. dbf2-3 (D128) alpha ade1 his1 trp2 dbf2-3 L. Johnston

1825. dbf3 (L124-11D) a ura3 dbf3 L. Johnston

1751. dbf3-1 (D128) alpha ade1 his1 trp2 dbf3-1 L. Johnston

1747. dbf8-1 (D128) alpha ade1 his1 trp2 dbf8-1 L. Johnston

1748. dbf9-1 (D128) alpha ade1 his1 trp2 dbf9-1 L. Johnston

1813. dbf10-1 (D141) alpha ade1 his1 trp2 dbf10-1 L. Johnston

1814. dbf11-1 (D132) alpha ade1 his1 trp2 dbf11-1 L. Johnston

1815. dbf13-1 (D101) alpha ade1 his1 trp2 dbf13-1 L. Johnston

1816. dbf14-1 (D22) alpha ade1 his1 trp2 dbf14-1 L. Johnston

1817. dbf14-2 (D25) alpha ade1 his1 trp2 dbf14-2 L. Johnston

1818. dbf14-3 (D44) alpha ade1 his1 trp2 dbf14-3 L. Johnston

1819. dbf15-1 (D22) alpha ade1 his1 trp2 dbf15-1 L. Johnston

1820. dbf20-1 (D175) alpha ade1 his1 trp2 dbf20-1 L. Johnston

1794. MH25 alpha/a dbf2/dbf2 gal1-D5/gal1-A ade1/+ his1/his1 trp2/trp2 +/ura1 +/tyr1 +/ade2 +/his L. Johnston

1795. MH26 alpha/a dbf3/dbf3 gal1-D5/gal1-a ade1/ade1 his1/+ trp2/+ +/lys2 +/ura1 +/tyr1 +/ade2 L. Johnston

1796. MH27 alpha/a dbf4/dbf4 gal1-D5/gal1-A ade1/ade1 his1/his1 trp2/+ +/lys2 +/tyr1 +/ade2 +/his7 L. Johnston

1621. g716-5a ho a can1 hom3-10 his1-7 L. Johnston

1622. 309 alpha ade2-R8 metX can1-11 L. Johnston

1717. L39-8C alpha trp1 or trp2 lys2 canR. L. Johnston

1628. 320 a rme ade2 ura3 leu1 can1-11 cyh2-21 L. Johnston

1716. alpha131-20 alpha ade2-R8 cyh2 can1 leu1 ura3 L. Johnston

807. x 464-20C alpha trp1 ade1 his2 leu1 gal1 J. F. T. Spencer

859. 168 a ade1 gal1 lys2 tyr1 his7 ura1 ade2 *Can. J. Microbiol.*, 1977, 23, 441 G.

Stewart
1789. L58.3b gal1 ade1 or ade2 L. Johnston
1638. L57-15b gal1 his7 lys2 tyr1 L. Johnston
1625. Z65 a/alpha gal1-1/gal1-4 lys2-1/lys2-2 tyr1-1/tyr1-2 his7-2/his7-1 ade1/+ +/ade2 +/ura L. Johnston
1757. M1-2B (YNN 27) alpha trp1 ura3-52 gal2 L. Johnston
865. 205 alpha gal7 lys2 tyr1 his4 leu2 thr4 MAL2 trp1 ade6 arg4 ura4 suc- *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
866. 206 a gal7 lys2 tyr1 his4 MAL2 trp1 ade6 arg4 suc- *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
1624. 108-3A a gal80 ade6 thr4 trp1 his3 rho- L. Johnston
1636. L53-14C a gal80 gal1-A tyr1 lys2 his7 ade1 (or ade2) ura1 L. Johnston
1635. L52-36 alpha gal80 gal1-D5 ade1 his1 (or his8) trp1 (or trp8) L. Johnston
1787. 106-3D alpha gal80 ura1 his1 L. Johnston
1634. MH10 alpha/a gal80/gal80 gal1-D5/gal1-A trp2/+ +/ura1 +/tyr1 +/lys2 +/his2 +/ade1 or 2 L. Johnston
867. 207 a ade1 gal1 ura3 his2 trp5 leu1 lys7 met2 MAL3 SUC2 *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
864. 194 a ade1 trp5 MAL6 suc- *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
862. 191 a ade2 MAL3 SUC3 MEL1 MGL2 MGL3 *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
861. 190 a his4 leu2 MAL2 suc- *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
863. 192 a trp1 ura3 MAL4 MEL1 MGL3 suc- gal3 gal4 *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
2252. a/alpha trp1/+ his2/+ ade1/+ STA2/STA2 *Biochem. J.*, 1988, 249, 163 I. Evans
860. 169 alpha ilv2 his FLO1FLO4) G. Stewart
868. 209 a ilv2 FLO1FLO4) G. Stewart
869. 209 alpha FLO1FLO4) G. Stewart
870. 210 a ade1 gal1 trp1 ura3 his2 leu1 met14 FLO1FLO4) G. Stewart
1391. sigma 1278b wild type (parent) *J. Bacteriol.*, 1970, 103, 770 R. Robbins
1390. 2512C a gap1 *J. Bacteriol.*, 1970, 103, 770 R. Robbins
1454. MP1, ATCC 42131 a/alpha ade2/+ his8/+ trp5-12/trp5-21 R. Fahrig
916. JCK5-5A alpha his4-A15 ade2-1 can(R) kar1-1 J. Conde
917. ABq 21 alpha his4-A15 ade2-1 can(R) kar1-2 nys(R) J. Conde
2266. BC3 leu2-3.112 trp1.1 ura3-52 pgk::TRP1 *Nucl. Acids Res.*, 1988, 16, 1333-1348 P. Piper
1639. a rad1 rad18 1799. CM31/1d alpha rad1 leu his ade lys L. Johnston
1800. CM26/4c rad4-3 his leu L. Johnston

1763. CM4/1d alpha rad5 ura L. Johnston
1764. CM5/1b alpha rad7 leu L. Johnston
1805. CM21/9a a rad9 ade arg leu lys L. Johnston
1806. CM30/2C alpha rad11 ade arg his leu L. Johnston
1801. CM1/8a alpha rad18 ade2 leu2 his4 L. Johnston
1640. g739-2a a rad50-1 can1 his1 ade2 (or adeX) L. Johnston
1721. g739-2d alpha rad50-1 hom3-10 his1 trp2 L. Johnston
1802. CM1/1C alpha rad51 lys2 leu2 his4 L. Johnston
1803. CM8/1a a rad54 ura his leu L. Johnston
1804. CM9/1a a rad55 leu his L. Johnston
1749. g725-12a alpha rad57-1 gal1-D5 hom3-10 his1-7 L. Johnston
1630. SK1 (L57.15b/L58.3b) gal1 het3 his7/+ lys2/+ tyr1/+ gal1-A/gal1-D5 +/ade1(or ade2) homothallic L. Johnston
1637. g761-10A [alpha]/g763-5c [a] rad51-3/rad51-3 gal1-A/gal1-5 his1-1/his1-7 +/his6 +/his7 tyr?/+ lys?/+ trp?/+ +/hom3-10 +/spo13-1 +/lys? +/tyr1 +/ura1 +/ade2
1792. g650-4a [alpha]/g650-12a[a] rad52-1/rad52-1 CAN(s)/can(R) +/hom3-10 +/his1-7 +/trp ade4/+ ho/ho
1745. ma3-3 (D43) alpha ade1 his1 trp2 rna3-3 L. Johnston
1746. ma3-4 (D167) alpha ade1 his1 trp2 rna3-4 L. Johnston
1758. ts96 alpha ade1 his1 trp2 ma11-2 dds1-1 L. Johnston
1614. K381-9D alpha spo11 ura3 ade6 arg4 aro7 asp5 met14 lys2 pet17 trp1 L. Johnston
1612. K382-19D alpha spo11 ura3 can1 cyh2 ade2 his7 hom3 tyr1 L. Johnston
1611. K382-23A a spo11 ura3 can1 cyh2 ade2 his7 hom3 L. Johnston
1616. K393-35C alpha spo11 ura3 his2 leu1 lys1 met4 pet8 L. Johnston
1617. K396-22B alpha spo11 ura3 ade1 his1 leu2 lys7 met3 trp5 L. Johnston
1613. K398-4D a spo11 ura3 ade6 arg4 aro7 asp5 met14 lys2 pet17 trp1 L. Johnston
1615. K399-7D a spo11 ura3 his2 leu1 lys1 met4 pet8 L. Johnston
227. Strain K, Manchester brewery strain, 1:5:4:2:1.
228. Strain R, Sheffield brewery strain, 5:1:1:3:5.
229. Strain T, London brewery strain, 5:1:1:4:5.
230. Strain U, Birmingham brewery strain, 5:1:1:4:5.
231. Strain V, Burton-on-Trent brewery strain, 1:5:5:3:1.
232. Strain S, American Yeast Foam, ATCC 60782, 1:1:3:5:1.
205. Hybrid 1 (NCYC 227 x NCYC 228)
206. Hybrid 2 (NCYC 227 x NCYC 229)
207. Hybrid 3 (NCYC 227 x NCYC 230)
208. Hybrid 4 (NCYC 227 x NCYC 230)
209. Hybrid 5 (NCYC 227 x NCYC 231)

210. Hybrid 6 (NCYC 227 x NCYC 231)
211. Hybrid 7 (NCYC 230 x NCYC 231)
212. Hybrid 15 (NCYC 227 x NCYC 232)
213. Hybrid 18 (NCYC 220 x NCYC 232)
214. Hybrid 24 (NCYC 222 x NCYC 221)
215. Hybrid 30 (NCYC 223 x NCYC 221)
216. Hybrid 38 (NCYC 224 x NCYC 226)
217. Hybrid 39 (NCYC 225 x NCYC 226)
218. Hybrid 48 (NCYC 226 x A162/1 ex NCYC 216)
219. Hybrid 64 (NCYC 227 x A162/3 ex NCYC 216)
220. Single spore isolate A2/3 strain from NCYC 212
221. Single spore isolate A38/3 strain from NCYC 213
222. Single spore isolate A48/1 strain from NCYC 213
223. Single spore isolate A85/1 strain from NCYC 214
224. Single spore isolate A101/1 strain from NCYC 214
225. Single spore isolate A101/2 strain from NCYC 214
226. Single spore isolate A104/1 strain from NCYC 214
646. x901-35C strain; alpha hom2 aro1A trp5 leu1 ade6 lys1 his6 ura1 arg4-1 thr1
647. x901-26A strain; alpha hom2 aro1A trp5 leu1 ade6 his6 ura1 arg4-2 thr1
648. x1069-1A strain; a ade1 his4 leu2 thr4 met2 trp5 ura1
650. DV 147 strain; alpha ade2, readily reverts to wild type
651. 4B strain; alpha his4 leu3 lys10(?) ade6 ade2 met(?),
652. S400D strain; a ilv1; has other unlisted requirements
653. S288C-27 strain; alpha ilv1, has other unlisted requirements
654. S2583D strain; alpha ilv2, has other unlisted requirements
655. S2582B strain; alpha ilv2, has other unlisted requirements
656. JB19 strain; alpha leu1 ade2
657. JB143 strain; alpha leu2 ade2
658. JA36 strain; a leu3 ade2 lys10
659. x 764 diploid hybrid strain; segregates for markers trp5 leu1 ade6 ura3 hom3 his6 lys1 arg4 mal1
660. x 373 tetraploid hybrid strain
661. x 362 hexaploid hybrid strain
663. xJ151 hybrid diploid strain; ATCC 60732; segregates for markers thr1 lys1 ura3 aro1A hom2 trp4 ade8; homozygous for ade2
664. xJ107 hybrid diploid strain; segregates for markers leu1 ura3 lys7 gal7 his8 ser1 ade2
264. S. Jackson Farmer's diploid strain 18, C53-8d x C24-13b) 1959

402. A. A. Eddy F28c strain, single spore isolate from NCYC 264) 1953

593. W. F. F. Oppenoorth (R7, O. Winge's C.L.303-9 hybrid strain) 1959

594. W. F. F. Oppenoorth (K83 S 58 hybrid strain) 1959

666. J. W. Millbank (respiratory deficient mutant derived from ale yeast NCYC 239) 1963

673. H. Laser (petite colony mutant by x-irradiation of baker's yeast) 1963

characterized by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

9. Genetically modified yeast *Saccharomyces cerevisiae* from one of the lines below:

505. CBS (1957). CBS 1171, ATCC 18824. Type strain for *Saccharomyces cerevisiae*. From brewing yeast. 5:1:5:5:1

70. A. C. Chapman (1933). *Saccharomyces anamensis*. NCTC 3864.

72. Schmitt (1924). *Saccharomyces brasiliensis*. 98 Carlsberg strain, NCTC 1808.

74. ATCC (1945). *Saccharomyces carlsbergensis*. ATCC 9080, ATCC 24904, CBS 2354.

76. A. C. Chapman (1933). *Saccharomyces cartilaginosus*. NCTC 3865.

77. A. Harden (1921). Baker's yeast strain. Requires thiamin, pantothenate and biotin (*Arch. Biochem.*, 1947, 14, 369. *J. Gen. Microbiol.*, 1983, 128, 2615-2620).

78. A. C. Chapman (1925). NCTC 2160

79. ATCC (1942). ATCC 7754, CBS 1368, NRRL Y-977, IFO 1346. Fleischmann baker's strain. Assay of biotin.

80. H. B. Hutchinson (1930). GB 354, NCTC 5922.

81. ATCC (1942). ATCC 7752, CBS 1320, NRRL Y-973, IFO 1234. Gebrüder Mayer Strain.

82. A. Klocker (1920). NCTC 466.

83. A. Harden (1920). Carlsberg Laboratory strain 21, NCTC 381.

84. H. J. Bunker (1945). NCTC 7043.

85. A. J. Kluyver (1939). NCTC 5916.

86. ATCC (1942). ATCC 7753, CBS 1321, NCTC 6421.

87. ATCC (1947). ATCC 9763, NRRL Y-567, CBS 2978, NCTC 10716 and NCTC 7239.

89. ATCC (1946). ATCC 7921. From Fleischmann yeast cake. (*J. Phys. Chem.*, 1928, 32, 1094).

90. A. Castellani (1928). NCTC 2779. Distiller's yeast.

91. A. Guilliermond (1925). *Saccharomyces chevalieri*. CBS 400, ATCC 9804, NCTC 2054. Type strain for *Saccharomyces chevalieri*. From wine.

92. A. C. Chapman (1933). *Saccharomyces delbrueckii*. NCTC 3964.

93. A. C. Chapman (1925). *Saccharomyces cerevisiae var. ellipsoideus*. NCTC 2161. Wine yeast.

94. A. Klocker (1920). *Saccharomyces ellipsoideus*. NCTC 467, NRRL Y-129, ATCC 2338.

95. A. C. Chapman (1933). *Saccharomyces ellipsoideus var. cratericus*. NCTC 3866.

96. M. B. Church (1922). *Saccharomyces cerevisiae var. ellipsoideus*. NCTC 1344. For the production of vinegar from apple juice.

97. H. B. Hutchinson (1945). *Saccharomyces ellipsoideus*. Michigan 48 strain. ATCC 10824, NCTC 7040.

99. J. L. Baker (1930). *Saccharomyces festinans*. From infected ale. (*J. Inst. Brew.*, 1929, 35, 466).

104. M. Kir (1934). Hungarian Wine Yeast.

107. A. J. Kluyver (1939). *Saccharomyces intermedius*.

108. T. Castelli (1939). *Saccharomyces italicus*. From Chianti grape must.

109. Carlsberg Laboratory (1924). *Saccharomyces lactis*.

110. A.Guilliermond (1925). *Saccharomyces lindneri*. CBS 403. From West African ginger beer.

113. A. Guilliermond (1925). *Saccharomyces vini*.

118. Gray, McGill University (1932). *Saccharomyces sake*.

121. A. C. Chapman (1921). *Saccharomyces thermantitonum*.

122. B. von Euler (1921). *Saccharomyces thermantitonum*. (*Biochem. Z.*, 1919, 97, 156).

124. A. Klocker (1920). NRRL Y-2434 *Saccharomyces turbidans*. (*J. Inst. Brew.*, 1950, 56, 192).

125. A. Heinemann (1933). *Saccharomyces ellipsoideus*. (*Exp. Cell. Res.*, 1958, 15, 214).

126. A. Klocker (1920). *Saccharomyces validus*.

167. B. W. Hammer (1922). *Torula cremoris*. From fermented cream.

176. A. J. Kluyver (1934). *Zygosaccharomyces priorianus*.

177. Anheuser-Busch Inc., USA (1927). Californian wine yeast. (*J. Gen. Microbiol.*, 1982, 128, 2615-2620).

182. A. C. Chapman (1933). Fernbach 38 strain.

183. A. C. Chapman (1933). Fernbach 40 strain.

186. Ö. Winge via British Fermentation Products Ltd. (1942). Hybrid K471.

187. A. C. Chapman (1921). Kefir Yeast.

190. A. C. Chapman (1931). *Saccharomyces logos*. ATCC 60731, NCTC 3341. Killer character K1 (Antonie van Leeuwenhoek, 1978, 44, 59-77).

192. G. Johnson (1936). Melbourne No. 1 strain.

196. A. C. Chapman (1933). Yeast Race V.

197. Mehta (1925). Yeast Race II.

198. Institut für Garungsgewerbe (1925). Yeast Race XII.

199. A. C. Chapman (1921). Saaz Yeast. NCTC 906, ATCC 2704, NRRL Y-239. From

Bohemian brewery.

200. A. C. Thaysen (1920). Sternberg 675 strain. For production of glycerol.

201. R. M. Nattrass (1943). 61 strain.

202. Carlsberg Laboratory (1924). Wine yeast, Johannesburg II Wortmann 76 strain.

232. R. S. W. Thorne (1951).

S, American Yeast Foam. 1:1:3:5:1 ATCC 60782. Killer character K1 (Antonie van Leeuwenhoek, 1978, 44, 59-77; *J. Ferm. Technol.*, 1985, 63, 421-429).

235. B. M. Brown (1951). Whitbread strain. ATCC 60733. Killer character K1 (Antonie van Leeuwenhoek, 1978, 44, 59-77). 5:1:4:4:1.

244. CMI (1951). *Saccharomyces intermedius*. IMI 46336.

252. S. Jackson (1961). *Saccharomyces ellipsoideus*. Strain 6.

291. S. Jackson via C. C. Lindegren (1951). Mrak 93 strain.

311. S. Jackson (1951). Benskin's brewery strain 65.

325. A. E. Wiles (1951). T43 Yorkshire type yeast. (*J. Inst. Brew.*, 1950, 56, 183).

341. A. E. Wiles (1951). From draught beer. 1:1:5:5:1

343. A. E. Wiles (1951). From draught beer. 1:1:5:5:1 (*J. Inst. Brew.*, 1950, 56, 183).

344. A. E. Wiles (1951). *Saccharomyces cerevisiae var. turbidans*. From draught beer. (*J. Inst. Brew.*, 1950, 56, 183).

345. A. E. Wiles (1951). *Saccharomyces cerevisiae var. turbidans*. From draught beer. (*J. Inst. Brew.*, 1950, 56, 183).

346. A. E. Wiles (1951). *Saccharomyces cerevisiae var. turbidans*. From draught beer. (*J. Inst. Brew.*, 1950, 56, 183).

356. C. H. Ridge (1953). Mead yeast.

357. T. Gray (1951). Avize-Cramant mead yeast.

358. T. Gray (1951). Plum mead yeast.

360. D. R. Jackson (1952). Seagram & Sons.

361. R. B. Gilliland (1952). *Saccharomyces diastaticus*. CBS 1782, NRRL Y-2416, ATCC 13007, IFO 1046. Type strain for *Saccharomyces diastaticus*. From brewer's wort.

365. F. W. Beech (1952). *Saccharomyces cerevisiae var. ellipsoideus*. From apple juice.

374. L. Hemmons (1953). *Saccharomyces oviformis*. From hazy ale.

394. A. A. Eddy (1954). *Saccharomyces chevalieri*.

406. R. B. Gilliland (1954). *Saccharomyces steineri*.

410. R. B. Gilliland (1954). *Saccharomyces fructuum*.

429. L. J. Wickerham (1955). Flor yeast. NRRL Y-2036.

430. L. J. Wickerham (1955). Riesling wine yeast. NRRL Y-2037.

431. L. J. Wickerham (1955). NRRL Y-132, ATCC 2345, ATCC 44732, NCYC 73.

447. J. S. Hough (1955). *Saccharomyces diastaticus*. From draught beer.

463. H. Aebi (1955). *Saccharomyces cerevisiae var. ellipsoideus*. Riesling wine yeast,

Herrliberg strain.

478. IFO (1956). Koykai 6 strain Sake yeast.

479. IFO (1956). Koykai 7 strain Sake yeast.

480. IFO (1956). R28. Awamori yeast.

481. IFO (1956). K71. Awamori yeast.

482. R. Barrington-Brock (1956). *Saccharomyces oviformis*. Champagne yeast, Moussec strain.

487. J. Lodder (1957). Single cell isolate from baking yeast. Requires inositol, pantothenate, biotin and thiamin.

488. J. Lodder (1957). Single cell isolate from baking yeast. Requires inositol, pantothenate and biotin; used in copper resistance studies (*Trans. Brit. Mycol. Soc.*, 1981, 77, 27).

489. J. Lodder (1957). Single cell isolate from baking yeast. Requires inositol, pantothenate and biotin.

490. J. Lodder (1957). Single cell isolate from baking yeast.

491. J. Lodder (1957). Single cell isolate from baking yeast. Requires inositol, pantothenate, biotin and thiamin.

506. CBS (1957). *Saccharomyces cerevisiae var. ellipsoideus*. CBS 1395, NRRL Y-1529. Type strain for *Saccharomyces ellipsoideus*.

510. CBS (1957). *Saccharomyces validus*. CBS 1541. Type strain for *Saccharomyces validus*.

525. R. Ryden (1958). Baking yeast.

592. W. F. F. Oppenoorth (1959). *Saccharomyces chevalieri*. W332. Used as DNA donor. (Brauwissenschaft, 1959, 12, 103).

609. M. P. Scarr (1960). *Saccharomyces fructuum*. From West Indian molasses.

618. A. A. Eddy (1962). *Saccharomyces cartilis*.

619. CBS (1962). CBS 2184. Jerez sherry yeast from Feduchy.

620. CBS (1962). *Saccharomyces fructuum*. CBS 3012. Jerez sherry yeast from Feduchy.

621. CBS (1962). *Saccharomyces fructuum*. CBS 3013. Jerez sherry yeast from Feduchy.

625. R. B. Gilliland (1960). *Saccharomyces diastaticus*. Flocculent strain. Protoplast fusion studies (*Current Genet.*, 1983, 7, 159-164), studies on starch utilization (*Biochem. J.*, 1988, 249, 163).

626. CBS (1962). *Saccharomyces oviformis*. CBS 429, NRRL Y-1356, IFO 0262. Type strain for *Saccharomyces oviformis*.

667. ATCC (1963). LK2 G12, ATCC 12341. Study of fat synthesis (*J. Biochem.*, 1978, 83, 1109-1116;

671. F. W. Beech (1964). *Saccharomyces capensis*. AWRI 81. Sherry yeast.
672. F. W. Beech (1964). VY22. Sherry yeast.
673. H. Laser (1963). Petite colony mutant by X-ray irradiation of baking yeast.
684. H. J. Bunker (1965). *Saccharomyces ellipsoideus*. Steinberg wine yeast.
694. F. R. Elliot (1966). Hybrid baking yeast. Distillers strain DCL 2984 from Distillers Co. Ltd.
695. ATCC (1966). ATCC 9896. Fleischmann 139 strain.
700. CBS (1966). *Saccharomyces steineri*. CBS 423, NRRL Y-1536, ATCC 2367, IFO 0253. Type strain for *Saccharomyces steineri*. From wine.
703. S. C. Hall (1967). From draught beer. Non-fining yeast.
713. M. Richards (1967). *Saccharomyces diastaticus*. ATCC 36902. From draught beer.
716. E. Minárik (1968). Thermophilic strain.
726. R. B. Gilliland (1970). 1430 Gilliland Class IV. (*Bull. Anc. Etud. Brass. de Louvain*, 1970, p59).
727. R. B. Gilliland (1970). 1511 Gilliland Class I. (*Bull. Anc. Etud. Brass. de Louvain*, 1970, p59).
738. A. P. Maule (1972). ATCC 36900. From continuous fermentation plant.
739. L. Penasse (1972). From air. High sterol content.
748. B. E. Kirsop (1972). From "bees wine" culture.
753. B. H. Kirsop (1973). From NCYC 240. Unable to ferment maltotriose.
754. B. H. Kirsop (1973). From NCYC 240. Able to ferment maltotriose.
755. G. G. Stewart (1973). Labatt's A. (*Proc. Amer. Soc. Brew. Chem.*, 1972, 3, 1-176, 118).
756. G. G. Stewart (1973). Labatt's B. (*Proc. Amer. Soc. Brew. Chem.*, 1972, 3, 1-176, 118).
757. R. A. Coutts (1972). Used for infection of yeast protoplasts with tobacco mosaic virus (*Nature*, 1972, 240, 466).
760. N. Okafor (1973). *Saccharomyces capensis*. From palm wine.
761. N. Okafor (1973). *Saccharomyces capensis*. ATCC 36899. From palm wine.
767. I. Campbell (1974). *Saccharomyces prostoserdovii*. as CBS 5155. T
812. J. M. Haslam (1974). KD 115, a ole1.
816. A. V. Hood (1974). AWRI 729, CECT 11133. Known as Epernay yeast.
817. J. A. Barnett (1975). as CBS 1172, ATCC 6037.
826. ATCC (1976). ATCC 26109, X-2180.
853. ATCC (1976). ATCC 2601, CBS 679, NRRL Y-53.
873. M. Yamamura (1977). L strain. Opsonin assay. (*Immunology*, 1978, 34, 689).
912. R. B. Gilliland (1978). *Saccharomyces diastaticus*. C606.
913. R. B. Gilliland (1978). *Saccharomyces diastaticus*. C607.

914. R. B. Gilliland (1978). *Saccharomyces diastaticus*. C608.

919. H. R. Schulka (1979). NSI 113 HS. Spontaneous mutant from a distillery yeast.

922. B. H. Kirsop (1979). X18. Very flocculent killer strain from batch fermentation.

923. B. H. Kirsop (1979). X19. Non-flocculent killer strain from batch fermentation.

933. J. Atputharajah (1979). *Saccharomyces chevalieri*. CRI 30. From toddy.

934. J. Atputharajah (1979). *Saccharomyces chevalieri*. CR1 Y11. From toddy.

935. J. Atputharajah (1979). *Saccharomyces chevalieri*. CR1 170. From toddy.

990. Chivas Bros Ltd (1981). *Saccharomyces diastaticus*.

991. Chivas Bros Ltd (1981). *Saccharomyces diastaticus*.

994. Chivas Bros Ltd (1981). *Saccharomyces diastaticus*. From bottled red wine.

995. S. I. Lesaffre et Cie (1981). Hybrid baking yeast. (U. S. Patent 4,396,632).

996. S. I. Lesaffre et Cie (1981). Hybrid baking yeast. (U. S. Patent 4,396,632).

999. All-Union Collection of Non-pathogenic Microorganisms (1981). Strain 383, Fleischmann Yeast Race xii, No. 46.

1370. B. E. Kirsop (1981). From wine packing cellar. Sporulates abundantly.

1379. New Zealand brewery (1981). Wild yeast.

1380. New Zealand brewery (1981). Wild yeast.

1406. S. Hara (1981). WL-7, IAM 4098 (*Agric. Biol. Chem.*, 1981, 45, 1327-1324. *Am. J. Enol. Vitic.*, 1980, 31, 28-37).

1407. S. Hara (1981). KL-88 Killer, sake strain. (*Agric. Biol. Chem.*, 1981, 45, 1327-1324. *Am. J. Enol. Vitic.*, 1980, 31, 28-37).

1408. S. Hara (1981). OC-2, IAM 4274. Mesophilic wine yeast. (*Agric. Biol. Chem.*, 1981, 45, 1327-1324. *Am. J. Enol. Vitic.*, 1980, 31, 28-37).

1409. S. Hara (1981). 2HYL-2. Hybrid NCYC 1406 x 1407. (*Agric. Biol. Chem.*, 1981, 45, 1327-1324. *Am. J. Enol. Vitic.*, 1980, 31, 28-37).

1410. S. Hara (1981). HY-1. Hybrid NCYC 1408 x 1407. (*Agric. Biol. Chem.*, 1981, 45, 1327-1324. *Am. J. Enol. Vitic.*, 1980, 31, 28-37).

1411. DSM (1982). DSM 70466. Bordeaux strain.

1412. DSM (1982). DSM 70461. Madeira strain.

1413. DSM (1982). DSM 70467. Sauternes strain.

1414. DSM (1982). DSM 70464. Tarragona strain.

1415. DSM (1982). DSM 70468. Tokay strain.

1431. C. Tusting (1982). French cider yeast.

1451. Weston Research Labs (1982).

1499. G. G. Stewart (1983). BB17. From Labatt's brewery.

1516. British brewery (1984).

1529. CBS (1984). CBS 6128. Baker's Yeast.

1530. CBS (1984). CBS 6131. Baker's Yeast.

1533. G. M. Gadd (1984). ED 66.20a.
1534. G. M. Gadd (1984).
1593. ATCC (1986). ATCC 60530.
1765. D. H. Grout (1987) ATCC 96819.
2551. K. Hickson (1994). From 'Teff'.
2589. CBS (1994). *Saccharomyces cf. cerevisiae*. CBS 426. From honey.
2593. M. Rhymes (1994). Flocculent isolate from NCYC 1168.
2645. British brewery (1994).
2657. Yogurt manufacturer (1994).
2740. CECT (1997). CECT 1170, DCL 740.
2743. CECT (1997). CECT 1482, IFI 460.
2776. F. C. Odds (1997). MAS 1.
2777. F. C. Odds (1997). MAS 2.
2778. F. C. Odds (1997). MAS 3.
2779. F. C. Odds (1997). MAS 4.
2780. F. C. Odds (1997). MAS 5.
2798. F. C. Odds (1997). MAS 6.
2799. CBS (1997). CBS 2247, CL 504, CCRC 21961, DBVPG 6172, IFO 1991, NRRL YB-4237, NRRL YB-4254, VKPM Y 47.
2826. CECT (1998). CECT 1483, IFI 649.
2830. CECT (1998). CECT 1683, IFI 270.
2843. UK Food Industry (1998).
2847. F. C. Odds (1999). J980380.

characterized by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

10. Genetically modified yeast *Saccharomyces cerevisiae* **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

11. Genetically modified yeast *Saccharomyces cerevisiae* **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by the following promoters (Mox, HSP30p, pMET3 or heterologous promoter) which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

12. Aerobic fermentation process with genetically modified yeast *Saccharomyces cerevisiae* **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by promoters which are

started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

13. Aerobic fermentation process with genetically modified yeast **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

14. Genetically modified microorganism **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by the promoter MOX or part of it, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

15. Genetically modified microorganism **characterized** by the fact that it can have the flocculation gene FLO10 regulated by the promoter MOX or part of it, which is started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

16. Aerobic fermentation process with a genetically modified microorganism **characterized** by the fact that it can have the flocculation gene PKC1, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

17. Aerobic fermentation process with a genetically modified microorganism **characterized** by the fact that it can have flocculation genes regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

18. Plasmid to be used in a genetically modified microorganism under fermentation process of claims 4 and 17, **characterized** by containing one or more of the following flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

19. Cassette to be used in a genetically modified microorganism of claims 4 and 17, **characterized** by containing one or more of the following flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

20. Vector to be used in a genetically modified microorganism of claims 4 and 17, **characterized** by containing one or more of the following flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

21. Plasmid to be used in a genetically modified microorganism under fermentation process of claims 5, 6, 7, 11, 14 and 15, **characterized** by containing one or more of the following flocculation genes, FLO1, FLO1S, FLO1L or FLO10, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

22. Cassette to be used in a genetically modified microorganism under fermentation process of claims 5, 6, 7, 8, 9, 10, 11, 14 and 15, **characterized** by containing one or more of the following flocculation genes, FLO1, FLO1S, FLO1L or FLO10, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

23. Vector to be used in a genetically modified microorganism under fermentation process of claims 5, 6, 7, 8, 9, 10, 11, 14 and 15, **characterized** by containing one or more of the following flocculation genes, FLO1, FLO1S, FLO1L or FLO10, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

24. Genetically modified microorganism of claims 1 to 23, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started depending on the presence or lack of nutrients such as sugars and nitrogen in the medium.

25. Plasmid to be used in a genetically modified microorganism of claims 1 to 23, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started depending on the presence or lack of nutrients such as sugars and nitrogen in the medium.

26. Cassette to be used in a genetically modified microorganism of claims 1 to 23, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started depending on the presence or lack of nutrients such as sugars and nitrogen in the medium.

27. Vector to be used in a genetically modified microorganism of claims 1 to 24, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started depending on the presence or lack of nutrients such as sugars and nitrogen in the medium.

28. Genetically modified microorganism of claims 1 to 24, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started depending on the presence or lack of ethanol in the medium.

29. Plasmid to be used in a genetically modified microorganism of claims 1 to 23, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started depending on the presence or lack of ethanol in the medium.

30. Cassette to be used in a genetically modified microorganism of claims 1 to 23, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started depending on the presence or lack of ethanol in the medium.

31. Vector to be used in a genetically modified microorganism of claims 1 to 23, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started depending on the presence or lack of ethanol in the medium.

32. Genetically modified microorganism of claims 1 to 23, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started depending on the occurrence of thernal shock in the medium or pH fall.

33. Plasmid to be used in a genetically modified microorganism of claims 1 to 23, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started depending on the occurrence of thernal shock in the medium or pH fall.

34. Cassette to be used in a genetically modified microorganism of claims 1 to 23, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started depending on the occurrence of thernal shock in the medium or pH fall.

35. Vector to be used in a genetically modified microorganism of claims 1 to 23, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started depending on the occurrence of thernal shock in the medium or pH fall.

36. Genetically modified microorganism of claims 4, 6, 12, 13, 16, 17, 18, 19, 20, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34 and 35, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

37. Plasmid to be used in a genetically modified microorganism of claims 4, 6, 12, 13, 16, 17, 18, 19, 20, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 and 36, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

38. Cassette to be used in a genetically modified microorganism of claims 4, 6, 12, 13, 16, 17, 18, 19, 20, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 and 36, **characterized** by the fact that it can have flocculation genes

regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

39. Vector to be used in a genetically modified microorganism of claims 4, 6, 12, 13, 16, 17, 18, 19, 20, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 and 36, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

40. Genetically modified microorganism, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by one or more of the following promoters or part of them: HSP30p or pMET3, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

41. Plasmid to be used in a genetically modified microorganism of claim 40, **characterized** by the fact that it can have one or more of the flocculation genes: FLO1, FLO1S or FLO1L, regulated by one or more of the following promoters or part of them: HSP30p or pMET3, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

42. Cassette to be used in a genetically modified microorganism of claim 40, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by one or more of the following promoters or part of them: HSP30p or pMET3, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

43. Vector to be used in a genetically modified microorganism of claim 40, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1S or FLO1L, regulated by one or more of the following promoters or part of them: HSP30p ou pMET3, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

44. Genetically modified microorganism **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by the following promoter or part of it: Mox, which is started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

45. Plasmid to be used in a genetically modified microorganism of claim 44, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by the following promoter or part of it: Mox, which is started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

46. Cassette to be used in genetically modified microorganism of claim 44, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by the following promotor or part of it: Mox, which is started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

47. Vector to be used in a genetically modified microorganism of claim 44, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by the following promoter or part of it: Mox, which is started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

48. Genetically modified microorganism **characterized** by the fact that it can have the following flocculation gene: FLO10, regulated by one or more of the following promoters or part of them: HSP30p ou pMET3, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

49. Plasmid to be used in a genetically modified microorganism of claim 48, **characterized** by the fact that it can have the following flocculation gene: FLO10, regulated by one of the following promoters or part of them: HSP30p ou pMET3, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

50. Cassette to be used in a genetically modified microorganism of claim 48, **characterized** by the fact that it can have the following flocculation gene: FLO10, regulated by one of the following promoters or part of them: HSP30p ou pMET3, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

51. Vector to be used in a genetically modified microorganism of claim 48, **characterized** by the fact that it can have the following flocculation gene: FLO10, regulated by one of the following promoters or part of them: HSP30p ou pMET3, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

52. Genetically modified microorganism **characterized** by the fact that it can have the flocculation gene: FLO10, regulated by one of the following promoters or part of them: ADH ou Mox, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

53. Plasmid to be used in a genetically modified microorganism of claim 52, **characterized** by the fact that it can have the following flocculation gene: FLO10, regulated by one of the following promoters or part of them: ADH ou Mox, which are started, depending on characteristics of chemical composition of

the medium, pH or by physical excitations.

54. Cassette to be used in a genetically modified microorganism of claim 52, **characterized** by the fact that it can have the following flocculation gene: FLO10, regulated by one of the following promoters or part of them: ADH or Mox, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

55. Vector to be used in a genetically modified microorganism of claim 52, **characterized** by the fact that it can have the following flocculation gene: FLO10, regulated by one of the following promoters or part of them: ADH ou Mox, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

56. Genetically modified microorganism, **characterized** by the fact that it can have one of the following flocculation genes: sfl1ou, fsu1ou, fsu2ou, tup1ou, cyc8ou, cka2 or FMC1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

57. Plasmid to be used in a genetically modified microorganism of claim 56, **characterized** by the fact that it can have one or more of the following flocculation genes: sfl1ou, fsu1ou, fsu2ou, tup1ou, cyc8ou, cka2 or FMC1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

58. Cassette to be used in a genetically modified microorganism of claim 56, **characterized** by the fact that it can have one or more of the following flocculation genes: sfl1ou, fsu1ou, fsu2ou, tup1ou, cyc8ou, cka2 or FMC1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

59. Vector to be used in a genetically modified microorganism of claim 56, **characterized** by the fact that it can have one or more of the following flocculation genes: sfl1ou, fsu1ou, fsu2ou, tup1ou, cyc8ou, cka2 or FMC1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

60. Genetically modified microorganism of claim 1, preferrably comprised by yeasts from lines *Pichia pastoris*, *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*,

Candida utilis, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

61. Genetically modified non-wild microorganism **characterized** by the fact that it can have flocculation genes regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

62. Aerobic fermentation process by using a genetically modified microorganism of claims 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 14, 15, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60 and 61, **characterized** by producing proteins of interest.

63. Genetically modified beer yeast of line W204, **characterized** by the fact that it can have flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

64. Plasmid to be used in a genetically modified beer yeast of line W204 of claim 63, **characterized** by containing flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

65. Cassette to be used in a genetically modified beer yeast of line W204 of claim 63, **characterized** by containing flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

66. Vector to be used in a genetically modified beer yeast of line W204 of claim 63, **characterized** by containing flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

67. Genetically modified beer yeast of line W204 of claim 63, **characterized** by the fact that it can have one of the following flocculation genes FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

68. Cassette to be used in a genetically modified beer yeast

of line W204 of claims 63 and 67, **characterized** by the fact that it can have one of the following flocculation genes: FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

69. Plasmid to be used in a genetically modified beer yeast of line W204 of claims 63 and 67, **characterized** by the fact that it can have of the following flocculation genes: FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

70. Vector to be used in a genetically modified beer yeast of line W204 of claims 63 and 67, **characterized** by the fact that it can have of the following flocculation genes: FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter, which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

71. Aerobic fermentation process using a genetically modified beer yeast of line W204 of claims 63, 64, 65, 66, 67, 68, 69 and 70, **characterized** by producing proteins of interest.

72. Aerobic fermentation process for the production of proteins of interest by using a genetically modified beer yeast of line W204, **characterized** by the fact that said yeast can have the flocculation genes, FLO1S and FLO1L, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations, so that the microorganism is not a wild microorganism.

73. Genetically modified microorganism of claim 1, **characterized** by the fact that it can have flocculation genes regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations, so that the microorganism is not a wild microorganism.

74. Aerobic fermentation process for the production of proteins of interest by using a genetically modified microorganism, **characterized** by having the flocculation genes, FLO1 or FLO10, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations, so that the microorganism is not a wild microorganism.

75. Genetically modified microorganism **characterized** by the fact that it can have a flocculation gene PKC1 regulated by the promoters ADH, Mox, HSP30p or heterologous promoter, which are started, depending on characteristics of

chemical composition of the medium, pH or by physical excitations.

76. Plasmid to be used in a genetically modified microorganism of claim 75, **characterized** by containing the flocculation gene PKC1 regulated by promoters ADH, Mox, HSP30p or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

77. Cassette to be used in a genetically modified microorganism of claim 75, **characterized** by containing the flocculation gene PKC1 regulated by promoters ADH, Mox, HSP30p or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

78. Vector to be used in a genetically modified microorganism of claim 75, **characterized** by containing the flocculation gene PKC1 regulated by promoters ADH, Mox, HSP30p or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

79. Aerobic fermentation process for the production of proteins of interest, **characterized** by using a genetically modified microorganism of claim 75.

80. Anaerobic fermentation process for the production of proteins of interest, **characterized** by using a genetically modified microorganism of claim 75.

81. Genetically modified microorganism of claims 5, 7, 8, 9, 10, 21, 22 and 23, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

82. Plasmid to be used in a genetically modified microorganism of claims 5, 7, 8, 9, 10, 21, 22 and 23, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

83. Cassette to be used in a genetically modified microorganism of claims 5, 7, 8, 9, 10, 21, 22 and 23, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

84. Vector to be used in a genetically modified

microorganism of claims 5, 7, 8, 9, 10, 21, 22 and 23, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

85. Anaerobic fermentation process with a genetically modified yeast, preferrably from lines *Pichia pastoris*, *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S ou FLO1L, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

86. Anaerobic fermentation process with a genetically modified yeast from lines *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO2, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

87. Anaerobic fermentation process with a genetically modified yeast from lines *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO3, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

88. Anaerobic fermentation process with a genetically modified yeast from lines *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO4, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

89. Anaerobic fermentation process with a genetically modified yeast from lines *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO5, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

90. Anaerobic fermentation process with a genetically modified yeast from lines *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida*

lipolytica or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO6, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

91. Anaerobic fermentation process with a genetically modified yeast from lines *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO7, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

92. Anaerobic fermentation process with a genetically modified yeast from lines *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO8, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

93. Anaerobic fermentation process with a genetically modified yeast from lines *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO9, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

94. Anaerobic fermentation process with a genetically modified yeast from lines *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO7, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

95. Anaerobic fermentation process with a genetically modified yeast from lines *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO8, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

96. Anaerobic fermentation process with a genetically modified yeast from lines *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO9, regulated by promoters which are started, depending on

characteristics of chemical composition of the medium, pH or by physical excitations.

97. Anaerobic fermentation process with a genetically modified yeast from lines *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO10, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

98. Genetically modified alga **characterized** by the fact that it can have flocculation genes regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

99. Genetically modified protozoa **characterized** by the fact that it can have flocculation genes regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

100. Anaerobic fermentation process with genetically modified yeast from the line *Pichia pastoris*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO4, regulated by promoters which are started, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

101. Genetically modified bacteria **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

102. Genetically modified fungus **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

103. Genetically modified archae **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

104. Genetically modified yeast **characterized** by the fact that it can have one or more of the flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

105. Genetically modified yeast **characterized** by the fact that it can have the flocculation gene, FLO10, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by

physical excitations.

106. Genetically modified yeast, preferrably from the lines *Pichia pastoris*, *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

107. Genetically modified yeast, preferrably from the lines *Pichia pastoris*, *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have the flocculation gene, FLO10, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

108. Genetically modified yeast *Saccharomyces cerevisiae* from one of the lines below:

956. X2180-1A, ATCC 26786 a SUC2 mal gal2 CUP1 R. K. Mortimer

957. X2180-1B, ATCC 26787 alpha SUC2 mal gal2 CUP1 R. K. Mortimer

857. 158 a *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart

858. 159 alpha *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart

713. KIL-k2 From draught beer) Antonie van Leeuwenhoek, 1978, 44, 59 M. Richards

738. KIL-k2 (brewery contaminant) Antonie van Leeuwenhoek, 1978, 44, 59 A. P. Maule

761. KIL-k3 From palm wine), CBS 7903 *J. Ferm. Technol.*, 1985, 63, 421-429 N. Okafor

1001. KIL-k2 (brewing yeast) Antonie van Leeuwenhoek, 1978, 44, 59

1561. A8209B his4-864 KIL-k1 G. Fink via T. Young

958. X2928-3D-1A a ade1 gal1 leu1 his2 ura3 trp1 met14 R. K. Mortimer

959. X2928-3D-1C alpha ade1 gal1 leu1 his2 ura3 trp1 met14 R. K. Mortimer

1786. STX 147-4C alpha ade1 his7 tyr1 gal1 cly8 ade5 aro2 met13 lys5 trp5 cyh2 arg4 lys1 ura4 gal2 ade2 rad56 L. Johnston

1620. STX77-6C alpha gal1 his4 trp1 hom3 ura3 CUP1 ilv3 ade3 rad52 ma1 L. Johnston

1618. X4119-19C a his7 tyr1 cdc9 trp4 aro1B hom2 rad2 thr1 lys11 gal2 ade2 L. Johnston

1661. X4120-19D alpha lys2 leu2 pet14 rad(?) ma3 ade8 aro1D met10 ade5 leu1 CUP1 L. Johnston

1619. STX66-4A a rad18 lys4 trp1 prt3 CUP1 gal2 ade2 met2 pha2 L. Johnston

1617. K396-22B alpha spo11 ura3 ade1 his1 leu2 lys7 met3 trp5 L. Johnston

1614. K381-9D alpha spo11 ura3 ade6 arg4 aro7 asp5 met14 lys2 pet17 trp1 L. Johnston

1613. K398-4D a spo11 ura3 ade6 arg4 aro7 asp5 met14 lys2 pet17 trp1 L. Johnston

1611. K382-23A a spo11 ura3 can1 cyh2 ade2 his7 hom3 L. Johnston

1612. K382-19D alpha spo11 ura3 can1 cyh2 ade2 his7 hom3 tyr1 L. Johnston

1616. K393-35C alpha spo11 ura3 his2 leu1 lys1 met4 pet8 L. Johnston

1615. K399-7D a spo11 ura3 his2 leu1 lys1 met4 pet8 L. Johnston

1383. DBY 747, ATCC 44774 a leu2-3 leu2-112 his3-DELTA1 trp4-289 ura3-52 *Gene*, 1979, 8, 17-24. J. F. Makins

1392. MC16 alpha leu2-3 his4-712FS) SUF2 ade2-1 lys2-1 *Nature*, 1981, 275, 104. J. F. Makins

1445. LL20 alpha his3-11 his3-15 leu2-3 leu2-112 *J. Bacteriol.*, 1979, 140, 73-82 A. Coddington

1527. MD40/4C alpha leu2-3 leu2-112 his3-11 his3-15 ura2 trp1 CAN s B. Bowen

1528. AH22 a leu2-3 leu2-112 his4 canR B. Bowen

1627. D13-1A (YNN6) a trp1 his3-532 gal2 L. Johnston

1771. cdc9-1 (L89-6C) a cdc9-1 leu2 ade1 ade2 ura1 lys2 L. Johnston

804. D160 a ura3 his1 arg6 trp2 ade1 J. F. T. Spencer

805. A364A a ade1 ade2 ura1 his7 lys2 tyr1 gal1 *J. Mol. Biol.*, 1976, 105, 427-443 J. F. T. Spencer

806. x112 alpha ade8-2 trp5-2 lys2-1 ura1-1 J. F. T. Spencer

808. GRH1 a trp1 ade1 his7 ura1 gal1 G. Stewart

1395. S1896D a met7 trp1 leu1 ade1 gal1 gal2 pet R. K. Mortimer

1396. F33 alpha met7 gal2 pet R. K. Mortimer

1623. X2181-1B a gal1 his2 trp1 ade1

1626. CG379 ade+ alpha his7-2 leu2-3 leu2-112 trp1-289 ura3-52 (ade5 rev)

1631. g440-7C alpha ade4 trp1 L. Johnston

1632. D273-11A alpha ade1 his1 trp2 L. Johnston

1662. alpha arg met L. Johnston

1663. a arg met L. Johnston

1664. alpha/alpha arg 2μ + L. Johnston

1719. A364A rho- a ade1 ade2 ura1 his7 lys2 tyr1 gal1 rho- L. Johnston

1720. B635 a cyc1-115 his1-1 lys2-1 trp2 L. Johnston

1772. L126-R9 a leu2 hom3-10 his1 L. Johnston

1790. a/a arg his 2μ + L. Johnston

1812. L126-2B a leu2 hom3-10 his1 L. Johnston

1821. S13 a his4 ura1 trp5 gal2 L. Johnston

1822. S49 a his4 ura1 trp5 gal2 ade6 L. Johnston

1961. GRF18 alpha leu2-3 leu2-212 his3-11 his3-15 canR G. Fink via D. MacKenzie

1356. A 137 alpha pho80-2 *J. Bacteriol.*, 1973, 113, 727-738 A. Coddington

1357. A 138 a pho80-2 *J. Bacteriol.*, 1973, 113, 727-738 A. Coddington

828. a ade1 J. F. T. Spencer
829. alpha ade1 J. F. T. Spencer
1577. a ade1 leu1 B. Pearson
1652. a ade1 leu2 B. Pearson
830. a ade2 J. F. T. Spencer
802. alpha ade2 (lys) J. F. T. Spencer
832. a ade3 J. F. T. Spencer
833. alpha ade3 (ura) J. F. T. Spencer
834. a ade4 J. F. T. Spencer
835. alpha ade4 (ura) J. F. T. Spencer
836. a ade5 J. F. T. Spencer
837. alpha ade5 (ura) J. F. T. Spencer
838. a ade6 J. F. T. Spencer
839. alpha ade6 (trp) J. F. T. Spencer
840. a ade7 J. F. T. Spencer
841. alpha ade7 J. F. T. Spencer
842. a ade8 J. F. T. Spencer
843. alpha ade8 (lys trp) J. F. T. Spencer
1654. cdc3-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc3-1 L. Johnston
1642. cdc4-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc4-1 L. Johnston
1643. cdc5-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc5-1 L. Johnston
1723. cdc6-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc6-1 L. Johnston
1729. cdc7-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc7-1 L. Johnston
1730. cdc8-141 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc8-141 L. Johnston
1667. cdc8-198 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc8-198 L. Johnston
1771. cdc9-1 (L89-6C) a cdc9-1 leu2 ade1 ade2 ura1 lys2 L. Johnston
1788. cdc9-1 rev1 cdc9-1 rev1 L. Johnston
1672. cdc9-12 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-12 L. Johnston
1673. cdc9-13 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-13 L. Johnston
1791. cdc9-3 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-3 2μ+ L. Johnston
1731. cdc9-4 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-4 L. Johnston
1732. cdc9-6 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-6 L. Johnston
1807. cdc9-7 (L82-2B) a cdc9-7 trp1 lys2 his7 L. Johnston
1808. cdc9-7 (L94-4D) a cdc9-7 trp1 ura3 L. Johnston
1670. cdc9-7 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-7 L. Johnston
1633. cdc9-7 rho- cdc9-7 rho- L. Johnston
1671. cdc9-8 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc9-8 L. Johnston
1674. cdc10-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc10-1 L. Johnston

1655. cdc11-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc11-1 L. Johnston
1733. cdc12-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc12-1 L. Johnston
1734. cdc13-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc13-1 L. Johnston
1735. cdc14-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc14-1 L. Johnston
1736. cdc18-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc18-1 L. Johnston
1737. cdc19-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc19-1 L. Johnston
1738. cdc26-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc26-1 L. Johnston
1665. cdc28-4 L31-7a a cdc28-4 tyr1 L. Johnston
1675. cdc30-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc30-1 L. Johnston
1676. cdc31-1 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc31-1 L. Johnston
1722. cdc36-16 SR661-2 a cdc36-16 trp1-1 ura1 L. Johnston
1666. cdc37-1 SR672-1 a cdc37-1 ura1 cyh2 L. Johnston
1641. cdc39-1 SR665-1 alpha cdc39-1 met2 tyr1 cyh2 L. Johnston
1677. cdc41 a ade1 ade2 ura1 his7 lys2 tyr1 gal1 cdc41 L. Johnston
1753. cdc6 (MH18) cdc6/cdc6 gal1/gal1 ade1/ade1 +/ade2 his1/his7 trp2/+ +/ura1 +/lys2 +/tyr1 2µ+ L. Johnston
1754. cdc13 (MH20) cdc13/cdc13 gal1/gal1 ade1/ade1 +/ade2 his1/his7 trp2/+ +/ura1 +/lys2 +/tyr1 2µ+ L. Johnston
1752. cdc15-1 (MH15) cdc15-1/cdc15-1 gal1/gal1 ade1/ade1 +/ade2 his1/his7 trp2/+ +/ura1 +/lys2 +/tyr1 2µ+ L. Johnston
1755. cdc17 (MH21) cdc17/cdc17 gal1/gal1 ade1/ade1 +/ade2 his1/his7 trp2/+ +/ura1 +/lys2 +/tyr1 2µ+ L. Johnston
1756. cdc21 (MH21) cdc21/cdc21 gal1/gal1 ade1/ade1 +/ade2 his1/his7 trp2/+ +/ura1 +/lys2 +/tyr1 2µ+ L. Johnston
1718. JC2 (L31-9a [a]/L31-2c [alpha]) cdc9/cdc9 cdc28/cdc28 ade/+ tyr1/tyr/1 canR/+ +/his1 L. Johnston
1797. cdc36(MH30) alpha/a gal1/gal1 ade1/+ his1/+ trp2/+ +/trp1 +/ura1
961. 2C-4 alpha arg4-2/+ arg4-17/+ CUP1/+ thr1/+; rec5 leu1 trp5 trp1 his5 ade2 *Radiation Res.*, 1972, 49, 133 & 148 R. K. Mortimer
960. 2C-8 alpha arg4-2/+ arg4-17/+ CUP1/+ thr1/+; rec4 leu1 trp5 trp1 his5 ade2 *Radiation Res.*, 1972, 49, 133 & 148 R. K. Mortimer
1823. dbf1 (L123-8A) alpha trp1 ura3 dbf1 L. Johnston
1824. dbf2 (L119-7D) alpha trp? ura3 ade1 dbf2 L. Johnston
1750. dbf2-3 (D128) alpha ade1 his1 trp2 dbf2-3 L. Johnston
1825. dbf3 (L124-11D) a ura3 dbf3 L. Johnston
1751. dbf3-1 (D128) alpha ade1 his1 trp2 dbf3-1 L. Johnston
1747. dbf8-1 (D128) alpha ade1 his1 trp2 dbf8-1 L. Johnston
1748. dbf9-1 (D128) alpha ade1 his1 trp2 dbf9-1 L. Johnston

1813. dbf10-1 (D141) alpha ade1 his1 trp2 dbf10-1 L. Johnston
1814. dbf11-1 (D132) alpha ade1 his1 trp2 dbf11-1 L. Johnston
1815. dbf13-1 (D101) alpha ade1 his1 trp2 dbf13-1 L. Johnston
1816. dbf14-1 (D22) alpha ade1 his1 trp2 dbf14-1 L. Johnston
1817. dbf14-2 (D25) alpha ade1 his1 trp2 dbf14-2 L. Johnston
1818. dbf14-3 (D44) alpha ade1 his1 trp2 dbf14-3 L. Johnston
1819. dbf15-1 (D22) alpha ade1 his1 trp2 dbf15-1 L. Johnston
1820. dbf20-1 (D175) alpha ade1 his1 trp2 dbf20-1 L. Johnston
1794. MH25 alpha/a dbf2/dbf2 gal1-D5/gal1-A ade1/+ his1/his1 trp2/trp2 +/ura1 +/tyr1 +/ade2 +/his L. Johnston
1795. MH26 alpha/a dbf3/dbf3 gal1-D5/gal1-a ade1/ade1 his1/+ trp2/+ +/lys2 +/ura1 +/tyr1 +/ade2 L. Johnston
1796. MH27 alpha/a dbf4/dbf4 gal1-D5/gal1-A ade1/ade1 his1/his1 trp2/+ +/lys2 +/tyr1 +/ade2 +/his7 L. Johnston
1621. g716-5a ho a can1 hom3-10 his1-7 L. Johnston
1622. 309 alpha ade2-R8 metX can1-11 L. Johnston
1717. L39-8C alpha trp1 or trp2 lys2 canR. L. Johnston
1628. 320 a rme ade2 ura3 leu1 can1-11 cyh2-21 L. Johnston
1716. alpha131-20 alpha ade2-R8 cyh2 can1 leu1 ura3 L. Johnston
807. x 464-20C alpha trp1 ade1 his2 leu1 gal1 J. F. T. Spencer
859. 168 a ade1 gal1 lys2 tyr1 his7 ura1 ade2 *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
1789. L58.3b gal1 ade1 or ade2 L. Johnston
1638. L57-15b gal1 his7 lys2 tyr1 L. Johnston
1625. Z65 a/alpha gal1-1/gal1-4 lys2-1/lys2-2 tyr1-1/tyr1-2 his7-2/his7-1 ade1/+ +/ade2 +/ura L. Johnston
1757. M1-2B (YNN 27) alpha trp1 ura3-52 gal2 L. Johnston
865. 205 alpha gal7 lys2 tyr1 his4 leu2 thr4 MAL2 trp1 ade6 arg4 ura4 suc- *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
866. 206 a gal7 lys2 tyr1 his4 MAL2 trp1 ade6 arg4 suc- *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
1624. 108-3A a gal80 ade6 thr4 trp1 his3 rho- L. Johnston
1636. L53-14C a gal80 gal1-A tyr1 lys2 his7 ade1(or ade2) ura1 L. Johnston
1635. L52-36 alpha gal80 gal1-D5 ade1 his1 (or his8) trp1(or trp8) L. Johnston
1787. 106-3D alpha gal80 ura1 his1 L. Johnston
1634. MH10 alpha/a gal80/gal80 gal1-D5/gal1-A trp2/+ +/ura1 +/tyr1 +/lys2 +/his2 +/ade1 or 2 L. Johnston
867. 207 a ade1 gal1 ura3 his2 trp5 leu1 lys7 met2 MAL3 SUC2 *Can. J. Microbiol.*, 1977,

23, 441 G. Stewart
864. 194 a ade1 trp5 MAL6 suc- *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
862. 191 a ade2 MAL3 SUC3 MEL1 MGL2 MGL3 *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
861. 190 a his4 leu2 MAL2 suc- *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
863. 192 a trp1 ura3 MAL4 MEL1 MGL3 suc- gal3 gal4 *Can. J. Microbiol.*, 1977, 23, 441 G. Stewart
2252. a/alpha trp1/+ his2/+ ade1/+ STA2/STA2 *Biochem. J.*, 1988, 249, 163 I. Evans
860. 169 alpha ilv2 his FLO1FLO4) G. Stewart
868. 209 a ilv2 FLO1FLO4) G. Stewart
869. 209 alpha FLO1FLO4) G. Stewart
870. 210 a ade1 gal1 trp1 ura3 his2 leu1 met14 FLO1FLO4) G. Stewart
1391. sigma 1278b wild type (parent) *J. Bacteriol.*, 1970, 103, 770 R. Robbins
1390. 2512C a gap1 *J. Bacteriol.*, 1970, 103, 770 R. Robbins
1454. MP1, ATCC 42131 a/alpha ade2/+ his8/+ trp5-12/trp5-21 R. Fahrig
916. JCK5-5A alpha his4-A15 ade2-1 can(R) kar1-1 J. Conde
917. ABq 21 alpha his4-A15 ade2-1 can(R) kar1-2 nys(R) J. Conde
2266. BC3 leu2-3.112 trp1.1 ura3-52 pgk::TRP1 *Nucl. Acids Res.*, 1988, 16, 1333-1348 P. Piper
1639. a rad1 rad18 (+ other unlisted requirements) L. Johnston
1799. CM31/1d alpha rad1 leu his ade lys L. Johnston
1800. CM26/4c rad4-3 his leu L. Johnston
1763. CM4/1d alpha rad5 ura L. Johnston
1764. CM5/1b alpha rad7 leu L. Johnston
1805. CM21/9a a rad9 ade arg leu lys L. Johnston
1806. CM30/2C alpha rad11 ade arg his leu L. Johnston
1801. CM1/8a alpha rad18 ade2 leu2 his4 L. Johnston
1640. g739-2a a rad50-1 can1 his1 ade2 (or adeX) L. Johnston
1721. g739-2d alpha rad50-1 hom3-10 his1 trp2 L. Johnston
1802. CM1/1C alpha rad51 lys2 leu2 his4 L. Johnston
1803. CM8/1a a rad54 ura his leu L. Johnston
1804. CM9/1a a rad55 leu his L. Johnston
1749. g725-12a alpha rad57-1 gal1-D5 hom3-10 his1-7 L. Johnston
1630. SK1 (L57.15b/L58.3b) gal1 het3 his7/+ lys2/+ tyr1/+ gal1-A/gal1-D5 +/ade1 (or ade2) homothallic L. Johnston
1637. g761-10A [alpha]/g763-5c [a] rad51-3/rad51-3 gal1-A/gal1-5 his1-1/his1-7 +/his6 +/his7 tyr?/+ lys?/+ trp?/+ +/hom3-10 +/spo13-1 +/lys? +/tyr1 +/ura1 +/ade2
1792. g650-4a [alpha]/g650-12a[a] rad52-1/rad52-1 CAN(s)/can(R) +/hom3-10 +/his1-7

+/trp ade4/+ ho/ho
1745. ma3-3 (D43) alpha ade1 his1 trp2 rna3-3 L. Johnston
1746. ma3-4 (D167) alpha ade1 his1 trp2 rna3-4 L. Johnston
1758. ts96 alpha ade1 his1 trp2 rna11-2 dds1-1 L. Johnston
1614. K381-9D alpha spo11 ura3 ade6 arg4 aro7 asp5 met14 lys2 pet17 trp1 L. Johnston
1612. K382-19D alpha spo11 ura3 can1 cyh2 ade2 his7 hom3 tyr1 L. Johnston
1611. K382-23A a spo11 ura3 can1 cyh2 ade2 his7 hom3 L. Johnston
1616. K393-35C alpha spo11 ura3 his2 leu1 lys1 met4 pet8 L. Johnston
1617. K396-22B alpha spo11 ura3 ade1 his1 leu2 lys7 met3 trp5 L. Johnston
1613. K398-4D a spo11 ura3 ade6 arg4 aro7 asp5 met14 lys2 pet17 trp1 L. Johnston
1615. K399-7D a spo11 ura3 his2 leu1 lys1 met4 pet8 L. Johnston
227. Strain K, Manchester brewery strain, 1:5:4:2:1.
228. Strain R, Sheffield brewery strain, 5:1:1:3:5.
229. Strain T, London brewery strain, 5:1:1:4:5.
230. Strain U, Birmingham brewery strain, 5:1:1:4:5.
231. Strain V, Burton-on-Trent brewery strain, 1:5:5:3:1.
232. Strain S, American Yeast Foam, ATCC 60782, 1:1:3:5:1.
205. Hybrid 1 (NCYC 227 x NCYC 228)
206. Hybrid 2 (NCYC 227 x NCYC 229)
207. Hybrid 3 (NCYC 227 x NCYC 230)
208. Hybrid 4 (NCYC 227 x NCYC 230)
209. Hybrid 5 (NCYC 227 x NCYC 231)
210. Hybrid 6 (NCYC 227 x NCYC 231)
211. Hybrid 7 (NCYC 230 x NCYC 231)
212. Hybrid 15 (NCYC 227 x NCYC 232)
213. Hybrid 18 (NCYC 220 x NCYC 232)
214. Hybrid 24 (NCYC 222 x NCYC 221)
215. Hybrid 30 (NCYC 223 x NCYC 221)
216. Hybrid 38 (NCYC 224 x NCYC 226)
217. Hybrid 39 (NCYC 225 x NCYC 226)
218. Hybrid 48 (NCYC 226 x A162/1 ex NCYC 216)
219. Hybrid 64 (NCYC 227 x A162/3 ex NCYC 216)
220. Single spore isolate A2/3 strain from NCYC 212
221. Single spore isolate A38/3 strain from NCYC 213
222. Single spore isolate A48/1 strain from NCYC 213
223. Single spore isolate A85/1 strain from NCYC 214
224. Single spore isolate A101/1 strain from NCYC 214
225. Single spore isolate A101/2 strain from NCYC 214

226. Single spore isolate A104/1 strain from NCYC 214
646. x901-35C strain; alpha hom2 aro1A trp5 leu1 ade6 lys1 his6 ura1 arg4-1 thr1
647. x901-26A strain; alpha hom2 aro1A trp5 leu1 ade6 his6 ura1 arg4-2 thr1
648. x1069-1A strain; a ade1 his4 leu2 thr4 met2 trp5 ura1
650. DV 147 strain; alpha ade2, readily reverts to wild type
651. 4B strain; alpha his4 leu3 lys10(?) ade6 ade2 met(?),
leaky mutant disomic for chromosome III, mates and sporulates well
652. S400D strain; a ilv1; has other unlisted requirements
653. S288C-27 strain; alpha ilv1, has other unlisted requirements
654. S2583D strain; alpha ilv2, has other unlisted requirements
655. S2582B strain; alpha ilv2, has other unlisted requirements
656. JB19 strain; alpha leu1 ade2
657. JB143 strain; alpha leu2 ade2
658. JA36 strain; a leu3 ade2 lys10
659. x 764 diploid hybrid strain; segregates for markers trp5 leu1 ade6 ura3 hom3 his6 lys1 arg4 mal1
660. x 373 tetraploid hybrid strain
661. x 362 hexaploid hybrid strain
663. xJ151 hybrid diploid strain; ATCC 60732; segregates for markers thr1 lys1 ura3 aro1A hom2 trp4 ade8; homozygous for ade2
664. xJ107 hybrid diploid strain; segregates for markers leu1 ura3 lys7 gal7 his8 ser1 ade2
264. S. Jackson Farmer's diploid strain 18, C53-8d x C24-13b) 1959
402. A. A. Eddy F28c strain, single spore isolate from NCYC 264) 1953
593. W. F. F. Oppenoorth (R7, O. Winge's C.L.303-9 hybrid strain) 1959
594. W. F. F. Oppenoorth (K83 S 58 hybrid strain) 1959
666. J. W. Millbank (respiratory deficient mutant derived from ale yeast NCYC 239) 1963
673. H. Laser (petite colony mutant by x-irradiation of baker's yeast) 1963

characterized by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

109. Genetically modified yeast *Saccharomyces cerevisiae* from one of the lines below:

505. CBS (1957). CBS 1171, ATCC 18824.
70. A. C. Chapman (1933). *Saccharomyces anamensis*. NCTC 3864.
72. Schmitt (1924). *Saccharomyces brasiliensis*. 98 Carlsberg strain, NCTC 1808.
74. ATCC (1945). *Saccharomyces carlsbergensis*. ATCC 9080, ATCC 24904, CBS 2354.
76. A. C. Chapman (1933). *Saccharomyces cartilaginosus*. NCTC 3865.

77. A. Harden (1921). Baker's yeast strain.

78. A. C. Chapman (1925). NCTC 2160

79. ATCC (1942). ATCC 7754, CBS 1368, NRRL Y-977, IFO 1346.

80. H. B. Hutchinson (1930). GB 354, NCTC 5922.

81. ATCC (1942). ATCC 7752, CBS 1320, NRRL Y-973, IFO 1234.

82. A. Klocker (1920). NCTC 466.

83. A. Harden (1920). Carlsberg Laboratory strain 21, NCTC 381.

84. H. J. Bunker (1945). NCTC 7043.

85. A. J. Kluyver (1939). NCTC 5916.

86. ATCC (1942). ATCC 7753, CBS 1321, NCTC 6421.

87. ATCC (1947). ATCC 9763, NRRL Y-567, CBS 2978, NCTC 10716 and NCTC 7239.

89. ATCC (1946). ATCC 7921.

90. A. Castellani (1928). NCTC 2779. Distiller's yeast.

91. A. Guilliermond (1925). *Saccharomyces chevalieri.* CBS 400, ATCC 9804, NCTC 2054. Type strain for *Saccharomyces chevalieri.* From wine.

92. A. C. Chapman (1933). *Saccharomyces delbrueckii.* NCTC 3964.

93. A. C. Chapman (1925). *Saccharomyces cerevisiae var. ellipsoideus.* NCTC 2161. Wine yeast.

94. A. Klocker (1920). *Saccharomyces ellipsoideus.* NCTC 467, NRRL Y-129, ATCC 2338.

95. A. C. Chapman (1933). *Saccharomyces ellipsoideus var. cratericus.* NCTC 3866.

96. M. B. Church (1922). *Saccharomyces cerevisiae var. ellipsoideus.* NCTC 1344.

97. H. B. Hutchinson (1945). *Saccharomyces ellipsoideus.* Michigan 48 strain. ATCC 10824, NCTC 7040.

99. J. L. Baker (1930). *Saccharomyces festinans.*

104. M. Kir (1934). Hungarian Wine Yeast.

107. A. J. Kluyver (1939). Saccharomyces intermedius.

108. T. Castelli (1939). *Saccharomyces italicus.* From Chianti grape must.

109. Carlsberg Laboratory (1924). *Saccharomyces lactis.*

110. A.Guilliermond (1925). *Saccharomyces lindneri.* CBS 403.

113. A. Guilliermond (1925). *Saccharomyces vini.*

118. Gray, McGill University (1932). *Saccharomyces sake.*

121. A. C. Chapman (1921). *Saccharomyces thermantitonum.*

122. B.von Euler (1921). *Saccharomyces thermantitonum.* (*Biochem. Z.*, 1919, 97, 156).

124. A. Klocker (1920). NRRL Y-2434 *Saccharomyces turbidans.*

125. A. Heinemann (1933). *Saccharomyces ellipsoideus.* (*Exp. Cell. Res.*, 1958, 15, 214).

126. A. Klocker (1920). *Saccharomyces validus.*

167. B. W. Hammer (1922). *Torula cremoris.* From fermented cream.

176. A. J. Kluyver (1934). *Zygosaccharomyces priorianus.*

177. Anheuser-Busch Inc., U. S. A. (1927).

182. A. C. Chapman (1933). Fernbach 38 strain.

183. A. C. Chapman (1933). Fernbach 40 strain.

186. Ö. Winge via British Fermentation Products Ltd. (1942). Hybrid K471.

187. A. C. Chapman (1921). Kefir Yeast.

190. A. C. Chapman (1931). *Saccharomyces logos.* ATCC 60731, NCTC 3341.

192. G. Johnson (1936). Melbourne No. 1 strain.

196. A. C. Chapman (1933). Yeast Race V.

197. Mehta (1925). Yeast Race II.

198. Institut für Garungsgewerbe (1925). Yeast Race XII.

199. A. C. Chapman (1921). Saaz Yeast. NCTC 906, ATCC 2704, NRRL Y-239.

200. A. C. Thaysen (1920). Sternberg 675 strain. For production of glycerol.

201. R. M. Nattrass (1943). 61 strain.

202. Carlsberg Laboratory (1924). Wine yeast, Johannesburg II Wortmann 76 strain.

232. R. S. W. Thorne (1951).

S, American Yeast Foam. 1:1:3:5:1 ATCC 60782.

235. B. M. Brown (1951). Whitbread strain. ATCC 60733.

244. CMI (1951). *Saccharomyces intermedius.* IMI 46336.

252. S. Jackson (1961). *Saccharomyces ellipsoideus.* Strain 6.

291. S. Jackson via C. C. Lindegren (1951). Mrak 93 strain.

311. S. Jackson (1951). Benskin's brewery strain 65.

325. A. E. Wiles (1951). T43 Yorkshire type yeast. (*J. Inst. Brew.*, 1950, 56, 183).

341. A. E. Wiles (1951). From draught beer. 1:1:5:5:1

343. A. E. Wiles (1951). From draught beer. 1:1:5:5:1 (*J. Inst. Brew.*, 1950, 56, 183).

344. A. E. Wiles (1951). *Saccharomyces cerevisiae var. turbidans.*

345. A. E. Wiles (1951). *Saccharomyces cerevisiae var. turbidans.*

346. A. E. Wiles (1951). *Saccharomyces cerevisiae var. turbidans.*

356. C. H. Ridge (1953). Mead yeast.

357. T. Gray (1951). Avize-Cramant mead yeast.

358. T. Gray (1951). Plum mead yeast.

360. D. R. Jackson (1952). Seagram & Sons.

361. R. B. Gilliland (1952). *Saccharomyces diastaticus.* CBS 1782, NRRL Y-2416, ATCC 13007, IFO 1046. Type strain for *Saccharomyces diastaticus.* From brewer's wort.

365. F. W. Beech (1952). *Saccharomyces cerevisiae var. ellipsoideus.* From apple juice.

374. L. Hemmons (1953). *Saccharomyces oviformis.* From hazy ale.

394. A. A. Eddy (1954). *Saccharomyces chevalieri.*

406. R. B. Gilliland (1954). *Saccharomyces steineri.*

410. R. B. Gilliland (1954). *Saccharomyces fructuum.*

429. L. J. Wickerham (1955). Flor yeast. NRRL Y-2036.

430. L. J. Wickerham (1955). Riesling wine yeast. NRRL Y-2037.

431. L. J. Wickerham (1955). NRRL Y-132, ATCC 2345, ATCC 44732, NCYC 73.

447. J. S. Hough (1955). *Saccharomyces diastaticus.* From draught beer.

463. H. Aebi (1955). *Saccharomyces cerevisiae var. ellipsoideus.*

478. IFO (1956). Koykai 6 strain Sake yeast.

479. IFO (1956). Koykai 7 strain Sake yeast.

480. IFO (1956). R28. Awamori yeast.

481. IFO (1956). K71. Awamori yeast.

482. R. Barrington-Brock (1956). *Saccharomyces oviformis.*

487. J. Lodder (1957).

488. J. Lodder (1957).

489. J. Lodder (1957).

490. J. Lodder (1957). Single cell isolate from baking yeast.

491. J. Lodder (1957).

506. CBS (1957). *Saccharomyces cerevisiae var. ellipsoideus.* CBS 1395, NRRL Y-1529.

510. CBS (1957). *Saccharomyces validus.* CBS 1541.

525. R. Ryden (1958). Baking yeast.

592. W. F. F. Oppenoorth (1959). *Saccharomyces chevalieri.* W332.

609. M. P. Scarr (1960). *Saccharomyces fructuum.* From West Indian molasses.

618. A. A. Eddy (1962). *Saccharomyces cartilis.*

619. CBS (1962). CBS 2184. Jerez sherry yeast from Feduchy.

620. CBS (1962). *Saccharomyces fructuum.* CBS 3012.

621. CBS (1962). *Saccharomyces fructuum.* CBS 3013.

625. R. B. Gilliland (1960). *Saccharomyces diastaticus.* Flocculent strain.

626. CBS (1962). *Saccharomyces oviformis.* CBS 429, NRRL Y-1356, IFO 0262.

667. ATCC (1963). LK2 G12, ATCC 12341.

671. F. W. Beech (1964). *Saccharomyces capensis.* AWRI 81. Sherry yeast.

672. F. W. Beech (1964). VY22. Sherry yeast.

673. H. Laser (1963). Petite colony mutant by X-ray irradiation of baking yeast.

684. H. J. Bunker (1965). *Saccharomyces ellipsoideus.* Steinberg wine yeast.

694. F. R. Elliot (1966). Hybrid baking yeast. Distillers strain DCL 2984 695. ATCC (1966). ATCC 9896. Fleischmann 139 strain.

700. CBS (1966). *Saccharomyces steineri.* CBS 423, NRRL Y-1536, ATCC 2367, IFO 0253. Type strain for *Saccharomyces steineri.* From wine.

703. S. C. Hall (1967). From draught beer. Non-fining yeast.

713. M. Richards (1967). *Saccharomyces diastaticus.* ATCC 36902.

716. E. Minárik (1968). Thermophilic strain.

726. R. B. Gilliland (1970). 1430 Gilliland Class IV.

727. R. B. Gilliland (1970). 1511 Gilliland Class I.

738. A.P.Maule (1972). ATCC 36900.

739. L. Penasse (1972). From air. High sterol content.

748. B. E. Kirsop (1972). From "bees wine" culture.

753. B. H. Kirsop (1973). From NCYC 240. Unable to ferment maltotriose.

754. B. H. Kirsop (1973). From NCYC 240. Able to ferment maltotriose.

755. G. G. Stewart (1973). Labatt's A. (*Proc. Amer. Soc. Brew. Chem.*, 1972, 3, 1-176, 118).

756. G. G. Stewart (1973). Labatt's B. (*Proc. Amer. Soc. Brew. Chem.*, 1972, 3, 1-176, 118).

757. R.A.Coutts (1972).

760. N. Okafor (1973). *Saccharomyces capensis*. From palm wine.

761. N. Okafor (1973). *Saccharomyces capensis*. ATCC 36899.

767. I. Campbell (1974). *Saccharomyces prostoserdovii*. as CBS 5155.

812. J. M. Haslam (1974). KD 115, a ole1.

816. A. V. Hood (1974). AWRI 729, CECT 11133.

817. J. A. Barnett (1975). as CBS 1172, ATCC 6037.

826. ATCC (1976). ATCC 26109, X-2180.

853. ATCC (1976). ATCC 2601, CBS 679, NRRL Y-53.

873. M. Yamamura (1977). L strain. Opsonin assay. (*Immunology*, 1978, 34, 689).

912. R. B. Gilliland (1978). *Saccharomyces diastaticus*. C606.

913. R. B. Gilliland (1978). *Saccharomyces diastaticus*. C607.

914. R. B. Gilliland (1978). *Saccharomyces diastaticus*. C608.

919. H. R. Schulka (1979). NSI 113 HS. Spontaneous mutant from a distillery yeast.

922. B. H. Kirsop (1979). X18. Very flocculent killer strain from batch fermentation.

923. B. H. Kirsop (1979). X19. Non-flocculent killer strain from batch fermentation.

933. J. Atputharajah (1979). *Saccharomyces chevalieri*. CRI 30. From toddy.

934. J. Atputharajah (1979). *Saccharomyces chevalieri*. CR1 Y11. From toddy.

935. J. Atputharajah (1979). *Saccharomyces chevalieri*. CR1 170. From toddy.

990. Chivas Bros Ltd (1981). *Saccharomyces diastaticus*.

991. Chivas Bros Ltd (1981). *Saccharomyces diastaticus*.

994. Chivas Bros Ltd (1981). *Saccharomyces diastaticus*. From bottled red wine.

995. S. I. Lesaffre et Cie (1981). Hybrid baking yeast. (U. S. Patent 4,396,632).

996. S. I. Lesaffre et Cie (1981). Hybrid baking yeast. (U. S. Patent 4,396,632).

999. All-Union Collection of Non-pathogenic Microorganisms (1981). Strain 383, Fleischmann Yeast Race xii, No. 46.

1370. B. E. Kirsop (1981). From wine packing cellar. Sporulates abundantly.

1379. New Zealand brewery (1981).

1380. New Zealand brewery (1981).

1406. S. Hara (1981). WL-7, IAM 4098 (*Agric. Biol. Chem.*, 1981, 45, 1327-1324. *Am. J. Enol. Vitic.*, 1980, 31, 28-37).

1407. S. Hara (1981). KL-88 Killer, sake strain. (*Agric. Biol. Chem.*, 1981, 45, 1327-1324. *Am. J. Enol. Vitic.*, 1980, 31, 28-37).

1408. S. Hara (1981). OC-2, IAM 4274. Mesophilic wine yeast. (*Agric. Biol. Chem.*, 1981, 45, 1327-1324. *Am. J. Enol. Vitic.*, 1980, 31, 28-37).

1409. S. Hara (1981). 2HYL-2. Hybrid NCYC 1406 x 1407. (*Agric. Biol. Chem.*, 1981, 45, 1327-1324. *Am. J. Enol. Vitic.*, 1980, 31, 28-37).

1410. S. Hara (1981). HY-1. Hybrid NCYC 1408 x 1407. (*Agric. Biol. Chem.*, 1981, 45, 1327-1324. *Am. J. Enol. Vitic.*, 1980, 31, 28-37).

1411. DSM (1982). DSM 70466. Bordeaux strain.

1412. DSM (1982). DSM 70461. Madeira strain.

1413. DSM (1982). DSM 70467. Sauternes strain.

1414. DSM (1982). DSM 70464. Tarragona strain.

1415. DSM (1982). DSM 70468. Tokay strain.

1431. C. Tusting (1982). French cider yeast.

1451. Weston Research Labs (1982).

1499. G. G. Stewart (1983). BB17.

1516. British brewery (1984).

1529. CBS (1984). CBS 6128. Baker's Yeast.

1530. CBS (1984). CBS 6131. Baker's Yeast.

1533. G. M. Gadd (1984). ED 66.20a.

1534. G. M. Gadd (1984).

1593. ATCC (1986). ATCC 60530.

1765. D. H. Grout (1987) ATCC 96819.

2551. K. Hickson (1994). From 'Teff';

2589. CBS (1994). *Saccharomyces cf. cerevisiae*. CBS 426. From honey.

2593. M. Rhymes (1994).

2645. British brewery (1994).

2657. Yogurt manufacturer (1994).

2740. CECT (1997). CECT 1170, DCL 740.

2743. CECT (1997). CECT 1482, IFI 460.

2776. F. C. Odds (1997). MAS 1.

2777. F. C. Odds (1997). MAS 2.

2778. F. C. Odds (1997). MAS 3.

2779. F. C. Odds (1997). MAS 4.

2780. F. C. Odds (1997). MAS 5.

2798. F. C. Odds (1997). MAS 6.

2799. CBS (1997). CBS 2247, CL 504, CCRC 21961, DBVPG 6172, IFO 1991, NRRL YB-4237, NRRL YB-4254, VKPM Y 47. T.

2826. CECT (1998). CECT 1483, IFI 649.

2830. CECT (1998). CECT 1683, IFI 270.

2843. UK Food Industry (1998).

2847. F. C. Odds (1999). J980380. From Vaginal swab.

characterized by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

110. Genetically modified yeast *Saccharomyces cerevisiae* **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

111. Genetically modified yeast *Saccharomyces cerevisiae* **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by the following promoters: Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

112. Aerobic fermentation process with genetically modified yeast *Saccharomyces cerevisiae* **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

113. Aerobic fermentation process with genetically modified yeast **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

114. Genetically modified microorganism **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S or FLO1L, regulated by the promoter MOX or part of it, which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

115. Genetically modified microorganism **characterized** by the fact that it can have the flocculation gene FLO10 regulated by the promoter MOX or part of it, which is restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

116. Aerobic fermentation process with a genetically modified microorganism **characterized** by the fact that it can have the flocculation gene PKC1, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

117. Aerobic fermentation process with a genetically modified microorganism **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

118. Plasmid to be used in a genetically modified microorganism under fermentation process of claims 104 and 117, **characterized** by containing one or more of the following flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

119. Cassette to be used in a genetically modified microorganism of claims 104 and 117, **characterized** by containing one or more of the following flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

120. Vector to be used in a genetically modified microorganism of claims 104 and 117, **characterized** by containing one or more of the following flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

121. Plasmid to be used in a genetically modified microorganism under fermentation process of claims 105, 106, 107, 111, 114 and 115, **characterized** by containing one or more of the following flocculation genes, FLO1, FLO1S, FLO1L or FLO10, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

122. Cassette to be used in a genetically modified microorganism under fermentation process of claims 105, 106, 107, 108, 109, 110, 111, 114 and 115, **characterized** by containing one or more of the following flocculation genes, FLO1, FLO1S, FLO1L or FLO10, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

123. Vector to be used in a genetically modified microorganism under fermentation process of claims 105, 106, 107, 108, 109, 110, 111, 114 and 115, **characterized** by containing one or more of the following flocculation

genes, FLO1, FLO1S, FLO1L or FLO10, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

124. Genetically modified microorganism of claims 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on the presence or lack of nutrients such as sugars and nitrogen in the medium.

125. Plasmid to be used in a genetically modified microorganism of claims 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on the presence or lack of nutrients such as sugars and nitrogen in the medium.

126. Cassette to be used in a genetically modified microorganism of claims 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on the presence or lack of nutrients such as sugars and nitrogen in the medium.

127. Vector to be used in a genetically modified microorganism of claims 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on the presence or lack of nutrients such as sugars and nitrogen in the medium.

128. Genetically modified microorganism of claims 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on the presence or lack of ethanol in the medium.

129. Plasmid to be used in a genetically modified microorganism of claims 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on the presence or lack of ethanol in the medium.

130. Cassette to be used in a genetically modified microorganism of claims 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on the presence or lack of ethanol in the medium.

131. Vector to be used in a genetically modified microorganism of claims 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on the presence of lack of ethanol in the medium.

132. Genetically modified microorganism of claims 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on the occurrence of thermal shock in the medium or pH fall.

133. Plasmid to be used in a genetically modified microorganism of claims 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on the occurrence of thermal shock in the medium or pH fall.

134. Cassette to be used in a genetically modified microorganism of claims 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on the occurrence of thermal shock in the medium or pH fall.

135. Vector to be used in a genetically modified microorganism of claims 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on the occurrence of thermal shock in the medium or pH fall.

136. Genetically modified microorganism of claims 104, 106, 112, 113, 116, 117, 118, 119, 120, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134 and 135, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

137. Plasmid to be used in a genetically modified microorganism of claims 104, 106, 112, 113, 116, 117, 118, 119, 120, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135 and 136, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

138. Cassette to be used in a genetically modified

microorganism of claims 104, 106, 112, 113, 116, 117, 118, 119, 120, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135 and 136, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter, which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

139. Vector to be used in a genetically modified microorganism of claims 104, 106, 112, 113, 116, 117, 118, 119, 120, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135 and 136, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

140. Genetically modified microorganism, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by one or more of the following promoters or part of them: HSP30p or pMET3, which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

141. Plasmid to be used in a genetically modified microorganism of claim 140, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by one or more of the following promoters or part of them: HSP30p or pMET3 which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

142. Cassette to be used in a genetically modified microorganism of claim 140, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by one or more of the following promoters or part of them: HSP30p or pMET3 which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

143. Vector to be used in a genetically modified microorganism of claim 140, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by one or more of the following promoters or part of them: HSP30p or pMET3 which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

144. Genetically modified microorganism, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by the following promoter or part of it: Mox, which is restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

145. Plasmid to be used in a genetically modified microorganism of claim 144, **characterized** by the fact that it can have one or more of the

following flocculation genes: FLO1, FLO1S or FLO1L, regulated by the following promoter or part of it: Mox, which is restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

146. Cassette to be used in a genetically modified microorganism of claim 144, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by the following promoter or part of it: Mox, which is restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

147. Vector to be used in a genetically modified microorganism of claim 144, **characterized** by the fact that it can have one or more of the following flocculation genes: FLO1, FLO1S or FLO1L, regulated by the following promoter or part of it: Mox, which is restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

148. Genetically modified microorganism **characterized** by the fact that it can have the flocculation gene: FLO10, regulated by one of the following promoters or part of them: HSP30p or pMET3 which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

149. Plasmid to be used in a genetically modified microorganism of claim 148, **characterized** by the fact that it can have the following flocculation gene: FLO10, regulated by one of the following promoters or part of them: HSP30p or pMET3 which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

150. Cassette to be used in a genetically modified microorganism of claim 148, **characterized** by the fact that it can have the following flocculation gene: FLO10, regulated by one of the following promoters or part of them: HSP30p or pMET3 which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

151. Vector to be used in a genetically modified microorganism of claim 148, **characterized** by the fact that it can have the following flocculation gene: FLO10, regulated by one of the following promoters or part of them: HSP30p or pMET3 which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

152. Genetically modified microorganism **characterized** by the fact that it can have the flocculation gene: FLO10, regulated by one of the following promoters or part of them (ADH or Mox), which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

153. Plasmid to be used in a genetically modified microorganism of claim 152, **characterized** by the fact that it can have the following

flocculation gene: FLO10, regulated by one of the following promoters or part of them ADH or Mox, which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

154. Cassette to be used in a genetically modified microorganism of claim 152, **characterized** by the fact that it can have the following flocculation gene: FLO10, regulated by one or more of the following promoters or part of them ADH or Mox, which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

155. Vector to be used in a genetically modified microorganism of claim 152, **characterized** by the fact that it can have the following flocculation gene: FLO10, regulated by of the following promoters or part of them ADH or Mox, which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

156. Genetically modified microorganism, **characterized** by the fact that it can have one of the following flocculation genes: sfl1ou, fsu1ou, fsu2ou, tup1ou, cyc8ou, cka2 or FMC1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

157. Plasmid to be used in a genetically modified microorganism of claim 156, **characterized** by the fact that it can have one or more of the following flocculation genes: sfl1ou, fsu1ou, fsu2ou, tup1ou, cyc8ou, cka2 or FMC1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

158. Cassette to be used in a genetically modified microorganism of claim 156, **characterized** by the fact that it can have one or more of the following flocculation genes: sfl1ou, fsu1ou, fsu2ou, tup1ou, cyc8ou, cka2 or FMC1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

159. Vector to be used in a genetically modified microorganism of claim 156, **characterized** by the fact that it can have one of the following flocculation genes: sfl1ou, fsu1ou, fsu2ou, tup1ou, cyc8ou, cka2 or FMC1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

160. Genetically modified microorganism, preferrably yeasts

from lines *Pichia pastoris*, *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

161. Genetically modified non-wild microorganism **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

162. Aerobic fermentation process by using a genetically modified microorganism of claims 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 114, 115, 124, 128, 132, 136, 140, 144, 148, 152, 156, 160 and 161, **characterized** by producing proteins of interest.

163. Genetically modified beer yeast of line W204, **characterized** by the fact that it can have flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

164. Plasmid to be used in genetically modified beer yeast of line W204 of claim 163, **characterized** by containing flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

165. Cassette to be used in a genetically modified beer yeast of line W204 of claim 163, **characterized** by containing flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations

166. Vector to be used in a genetically modified beer yeast of line W204 of claim 163, characterized by containing flocculation genes, FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

167. Genetically modified beer yeast of line W204 of claim 163, **characterized** by the fact that it can have one of the following flocculation genes FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or

heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

168. Cassette to be used in a genetically modified beer yeast of line W204 of claims 163 and 167, **characterized** by the fact that it can have one of the following flocculation genes FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

169. Plasmid to be used in a genetically modified beer yeast of line W204 of claims 163 and 167, **characterized** by the fact that it can have one of the following flocculation genes FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

170. Vector to be used in a genetically modified beer yeast of line W204 of claims 163 and 167, **characterized** by the fact that it can have one of the following flocculation genes FLO2, FLO3, FLO4, FLO5, FLO6, FLO7, FLO8, FLO9, FLO11 or Lg-FLO1, regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

171. Aerobic fermentation process using a genetically modified beer yeast of line W204 of claims 163, 164, 165, 166, 167, 168, 169 and 170, **characterized** by producing proteins of interest.

172. Aerobic fermentation process for the production of proteins of interest by using genetically modified beer yeast of line W204, **characterized** by the fact that said yeast can have the flocculation genes, FLO1S and FLO1L, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations, so that the microorganism is not a wild microorganism.

173. Genetically modified microorganism of claim 101, **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations, so that the microorganism is not a wild microorganism.

174. Aerobic fermentation process for the production of proteins of interest by using a genetically modified microorganism, **characterized** by the having the flocculation genes, FLO1 or FLO10, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by

physical excitations, so that the microorganism is not a wild microorganism.

175. Genetically modified microorganism, **characterized** by the fact that it can have one flocculation gene PKC1 regulated by promoters: ADH, Mox, HSP30p or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

176. Plasmid to be used in a genetically modified microorganism of claim 175, characterized by containing the flocculation gene PKC1 regulated by promoters: ADH, Mox, HSP30p or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

177. Cassette to be used in a genetically modified microorganism of claim 175, **characterized** by containing the flocculation gene PKC1 regulated by promoters: ADH, Mox, HSP30p or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

178. Vector to be used in a genetically modified microorganism of claim 175, **characterized** by containing the flocculation gene PKC1 regulated by promoters: ADH, Mox, HSP30p or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

179. Aerobic fermentation process for the production of proteins of interest, **characterized** by using a genetically modified microorganism of claim 175.

180. Anaerobic fermentation process for the production of proteins of interest, **characterized** by using a genetically modified microorganism of claim 175.

181. Genetically modified microorganism of claims 105, 107, 108, 109, 110, 121, 122 and 123, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

182. Plasmid to be used in a genetically modified microorganism of claims 105, 107, 108, 109, 110, 121, 122, 123 and 181, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

183. Cassette to be used in a genetically modified

microorganism of claims 105, 107, 108, 109, 110, 121, 122, 123 and 181, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations

184. Vector to be used in a genetically modified microorganism of claims 105, 107, 108, 109, 110, 121, 122, 123 and 181, **characterized** by the fact that it can have flocculation genes regulated by one of the following promoters or part of them: ADH, Mox, HSP30p, pMET3 or heterologous promoter which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

185. Anaerobic fermentation process with a genetically modified yeast, from lines *Pichia pastoris*, *Hansenula polymorpha*, *Saccharomyces fragilis*, *Saccharomyces ellipsoideus*, *Saccharomyces calsbergensis*, *Candida utilis*, *Candida lipolytica* or *Kluyveromyces lactis*, **characterized** by the fact that it can have one or more of the flocculation genes, FLO1, FLO1S ou FLO1L, regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

186. Genetically modified alga **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.

187. Genetically modified protozoa **characterized** by the fact that it can have flocculation genes regulated by promoters which are restrained, depending on characteristics of chemical composition of the medium, pH or by physical excitations.